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	MS-GPC- 8-27-7	MS-GPC- 8-27-10	MS-GPC- 8-6-13	MS-GPC- 8-27-41	MS-GPC- 8-6-47	MS-GPC- 8-10-57	MS-GPC- 8-6-27	MS-GPC- 8	MS-GPC- 8-6
Plastic	-0.004	-0.020	-0.022	-0.025	-0.001	0.005	0.007	-0.022	-0.018
BSA	-0.003	-0.019	-0.021	-0.022	0.008	0.003	0.003	-0.016	-0.019
Testosterone									
-BSA	-0.005	-0.010	-0.012	-0.007	0.011	0.003	0.002	-0.009	-0.012
Lysozyme	-0.005	-0.079	-0.079	-0.073	0.013	0.014	0.006	-0.081	-0.072
human									
Apotransferrin	-0.009	-0.016	-0.018	-0.018	-0.005	-0.008	-0.004	-0.014	-0.016
MHCII (DRA*0101/ DRB1*0401)	1.549	1.493	1.467	1.525	1.400	1.256	1.297	1.058	1.306

Fig. 1A

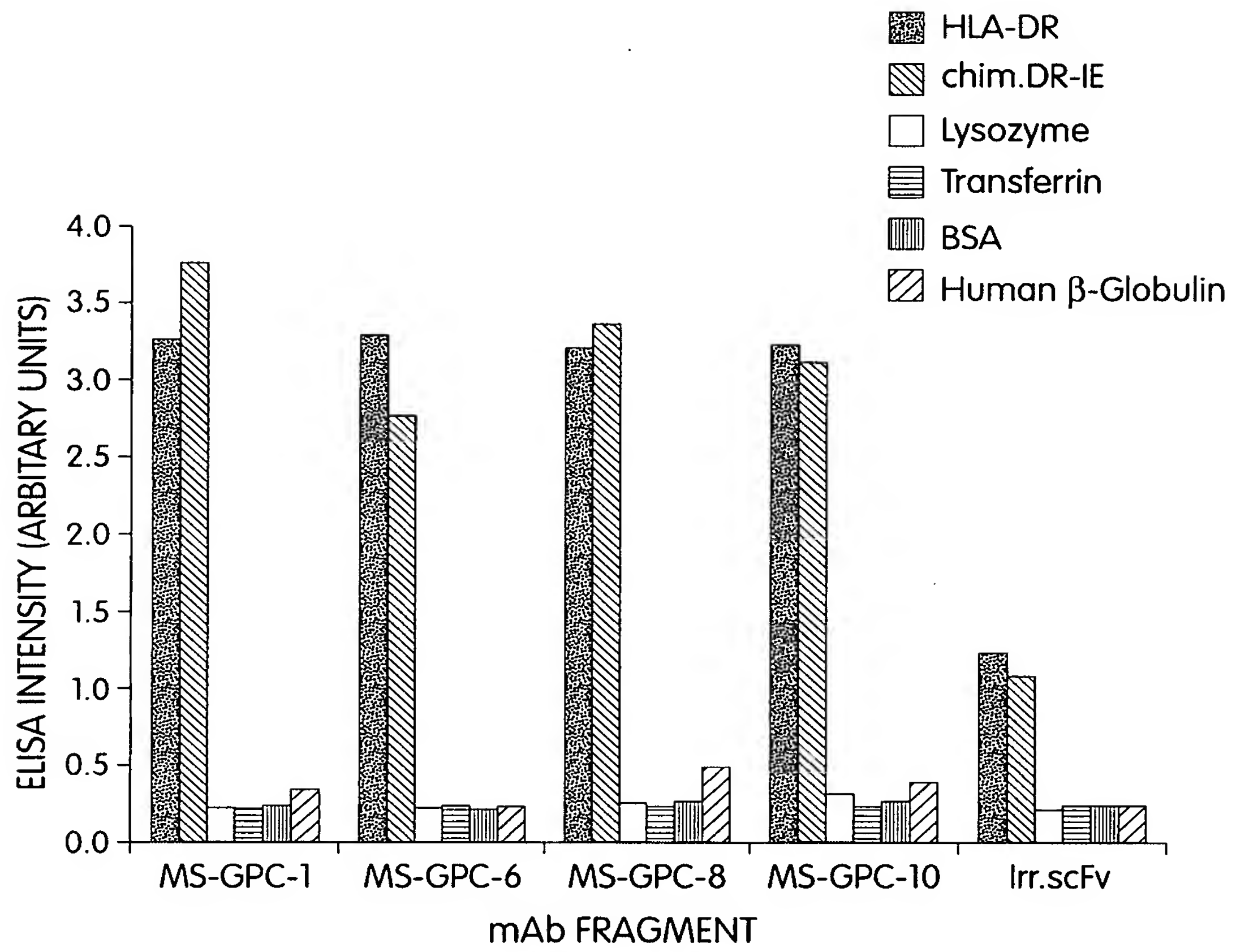


Fig. 1 B

Target Proteins	scFv													IgG		
	17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3	
DR4Dw4 Purified	+ <sup>a</sup>	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
Chimeric DR-IE purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
Lysozyme	- <sub>b</sub>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Transferrin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
BSA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Human gamma globulin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

a. In Elisa, OD (at 370 nm - background): > 1.5  
b. In Elisa, OD (at 370 nm - background): < 0.5

Fig. 1C

Cell Line	HLA-	DRB1*	scFv														IgG			
			17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3			
LG2	DR1	0101	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+			
E4181324	DR2	15021	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+			
VAVY	DR3	0301	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+			
PRIESS	DR4Dw4	0401	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+			
TS10	DR4Dw10	0402	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+			+/- <sup>c</sup>
BIN40	DR4Dw14	0404	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+			
TAB089	DR8	8031	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+			
DKB	DR9	9012	+	+	+/-	+/-	+	+	+	+	+	+	+	+	+	+	+			+/-
WT47	DR13	1302	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+			
TEM	DR14	1401	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+			
L105.1	DRw52	B3*0101	+	-	-	-	nt <sup>d</sup>	+	-	+	+	+	nt	nt	+	+/-	+/-			
L257.6	DRw53	B4*0101	+/-	-	+	-	nt	+	-	+	+/-	+/-	nt	nt	+	+	+			
L25.4	DPw4/w4.2	DP0103/0402	-	-	-	-	nt	+	-	-	-	-	nt	nt	+/-	-	+/-			
L256.12	DPw2/w2.1	DP0202/0201	-	-	-	-	nt	+/-	-	-	-	-	nt	nt	-	-	-			
L21.3	DQ7/w2	DQ0201/0602	-	-	-	-	nt	+	-	+	-	-	nt	nt	nt	nt	nt			
Target Cell			% Cells Killed <sup>e</sup>																	
PRIESS			75	20	28	32	22	89	33	59	75	34	1	5	88	93	74			

a. FACS analysis, mAb + FITC-anti human IgG<sub>4</sub>, mean fluorescence intensity > 30.  
b. Mean fluorescence intensity < 10.  
c. Mean fluorescence intensity 10-30.  
d. Not tested.  
e. Based on viable cell recovery after treatment with 200nM scFv plus 100 nM anti-FLAG or 50 nM mab at 37°C for 4h. Determined by light.

Fig. 2

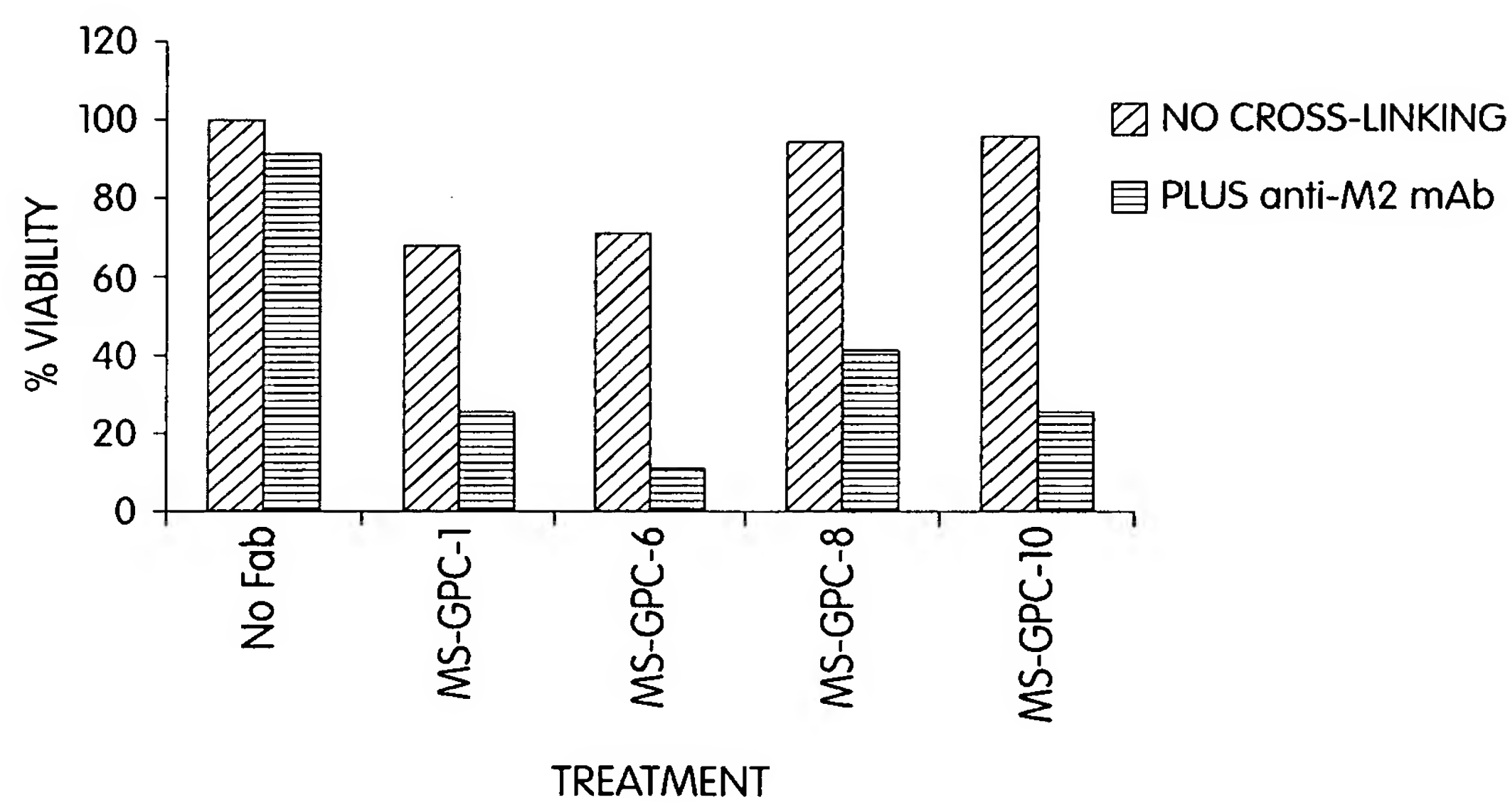


Fig. 3

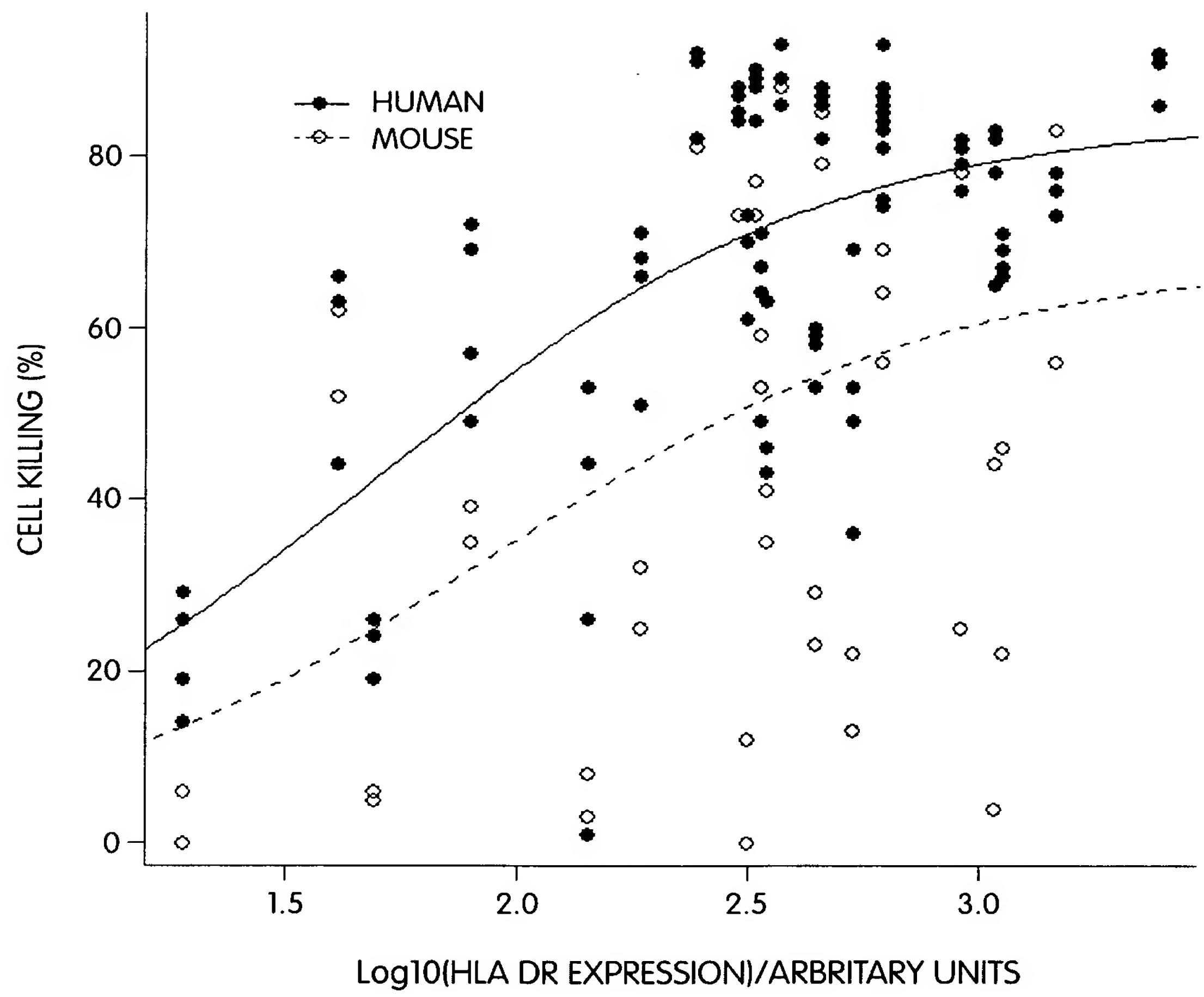


Fig. 4

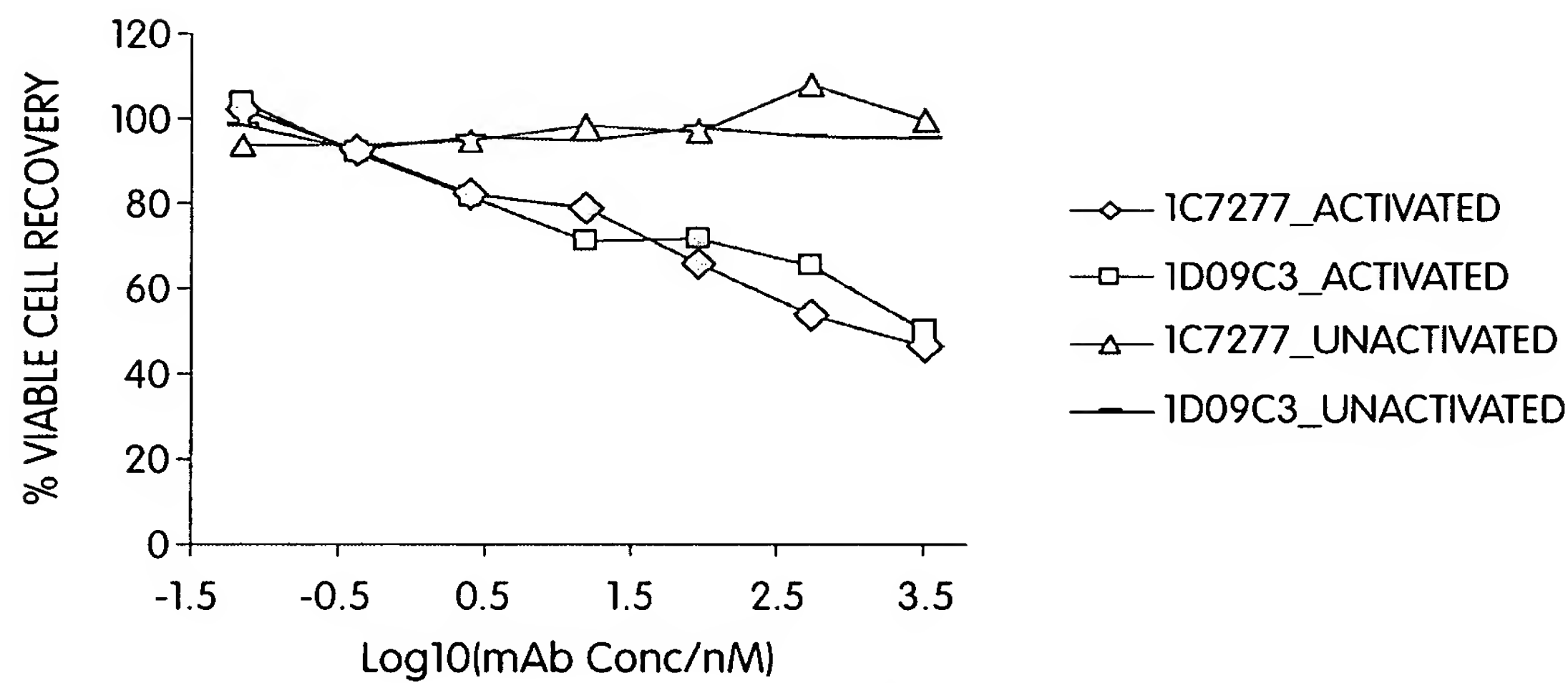


Fig. 5

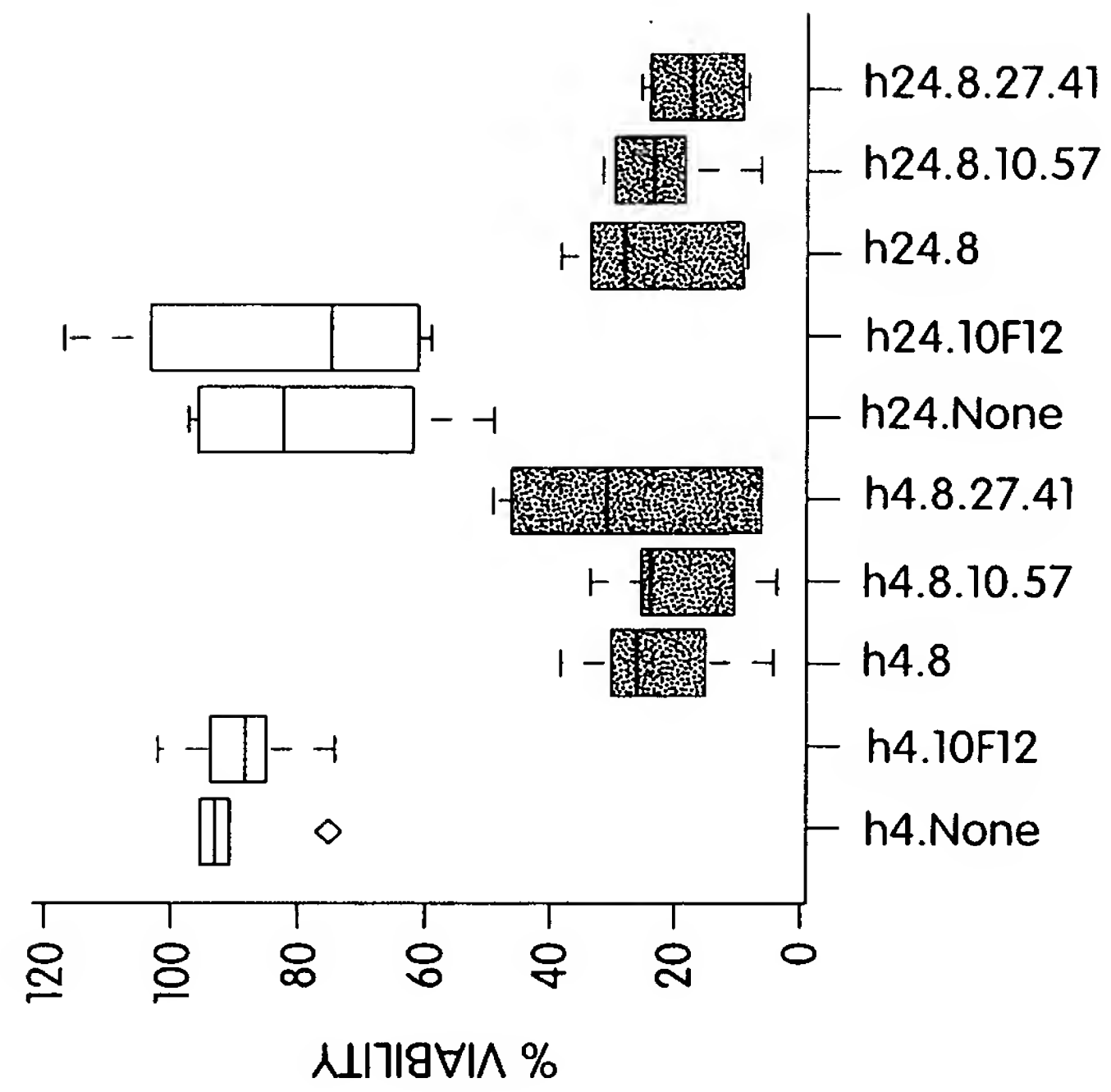
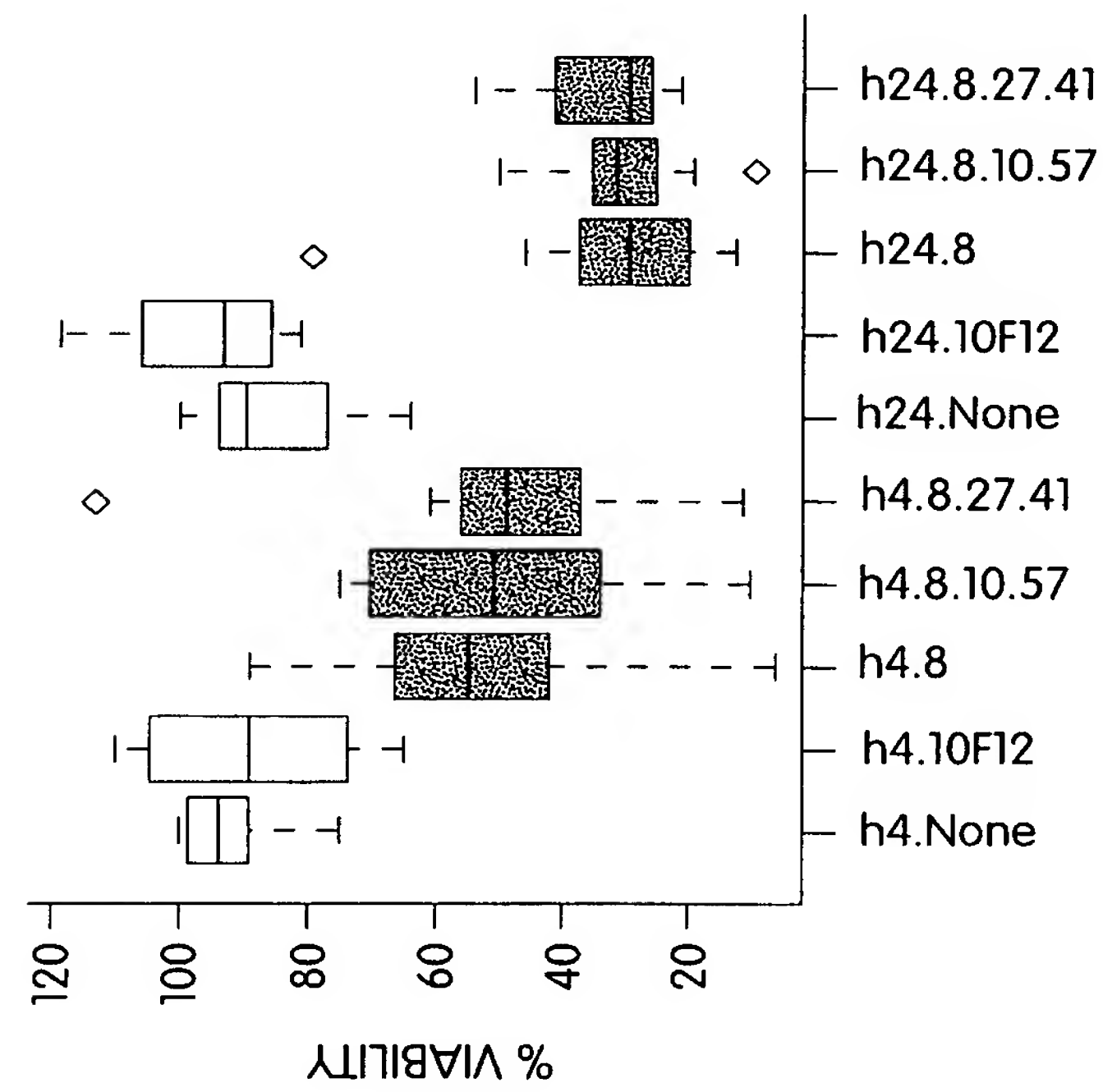
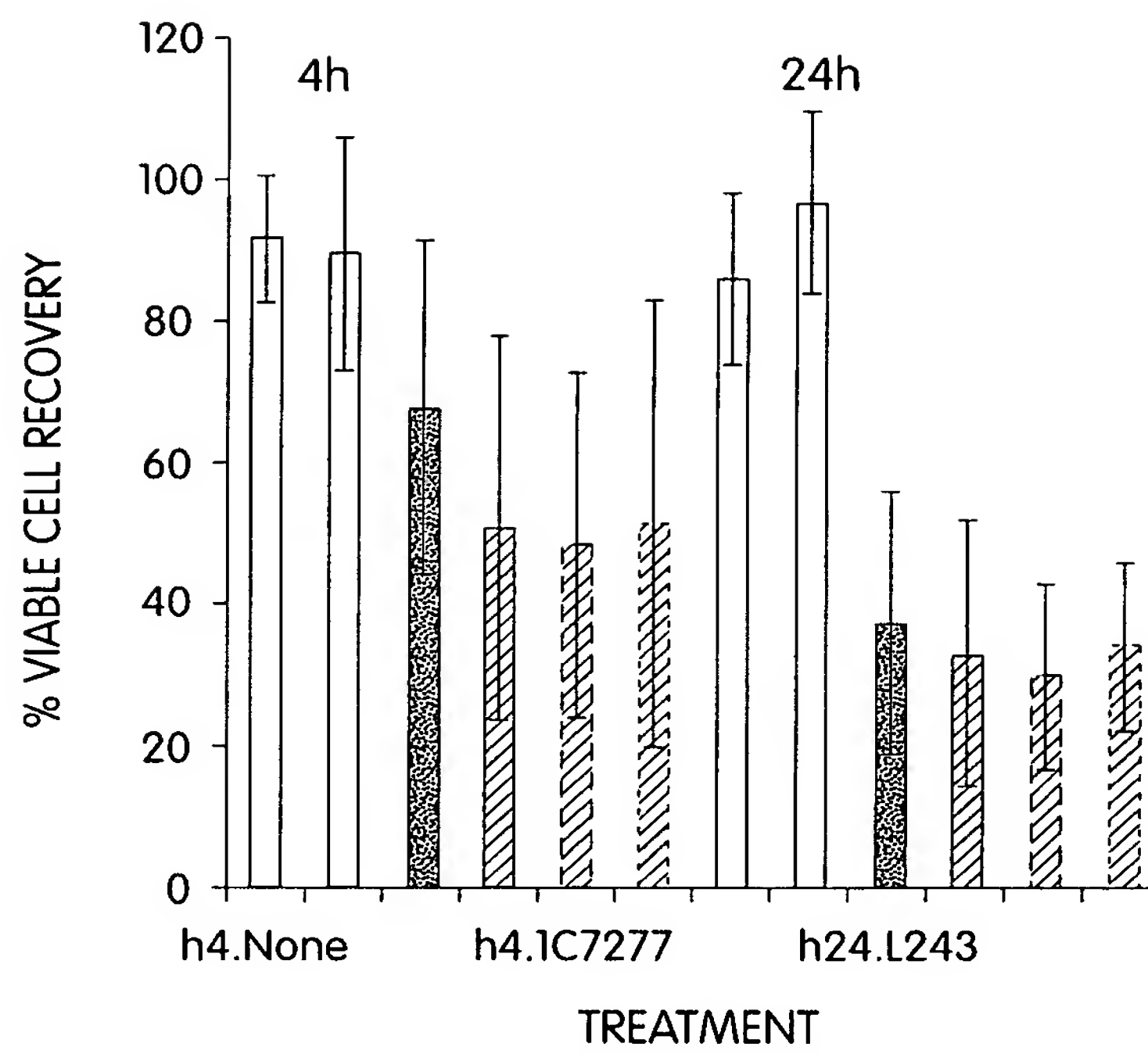


Fig. 6A





**Fig. 6B**

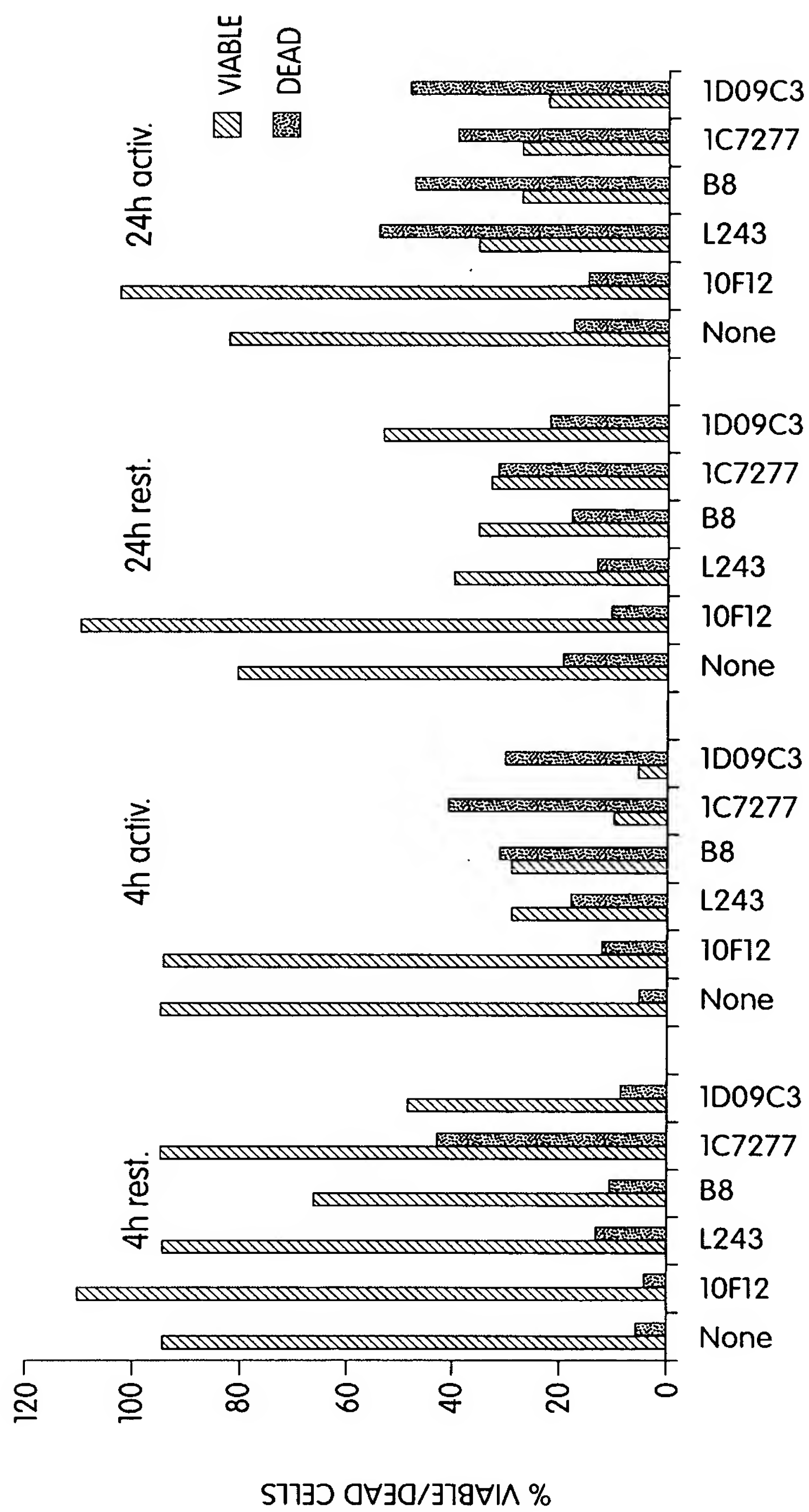


Fig. 6C

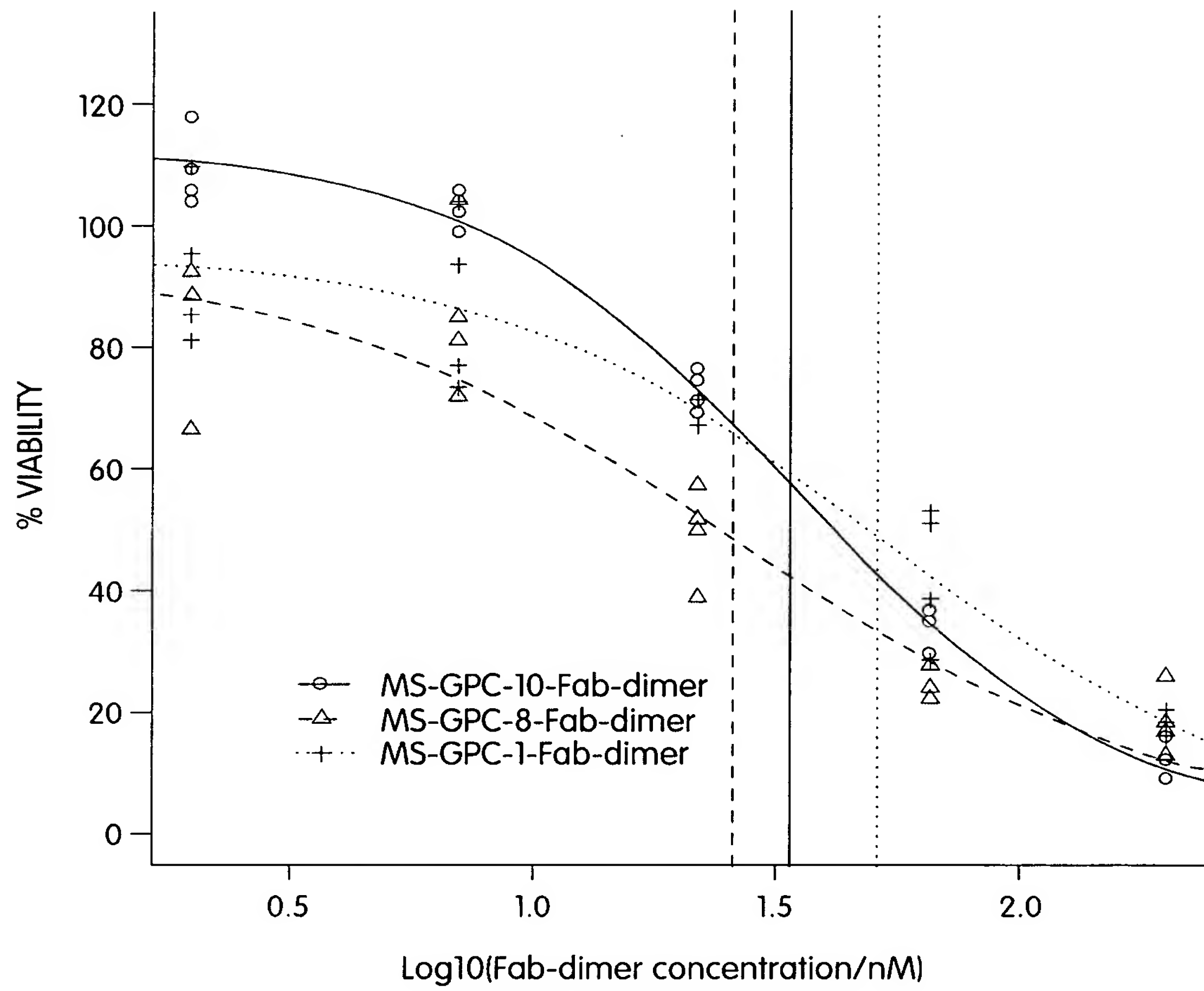


Fig. 7A

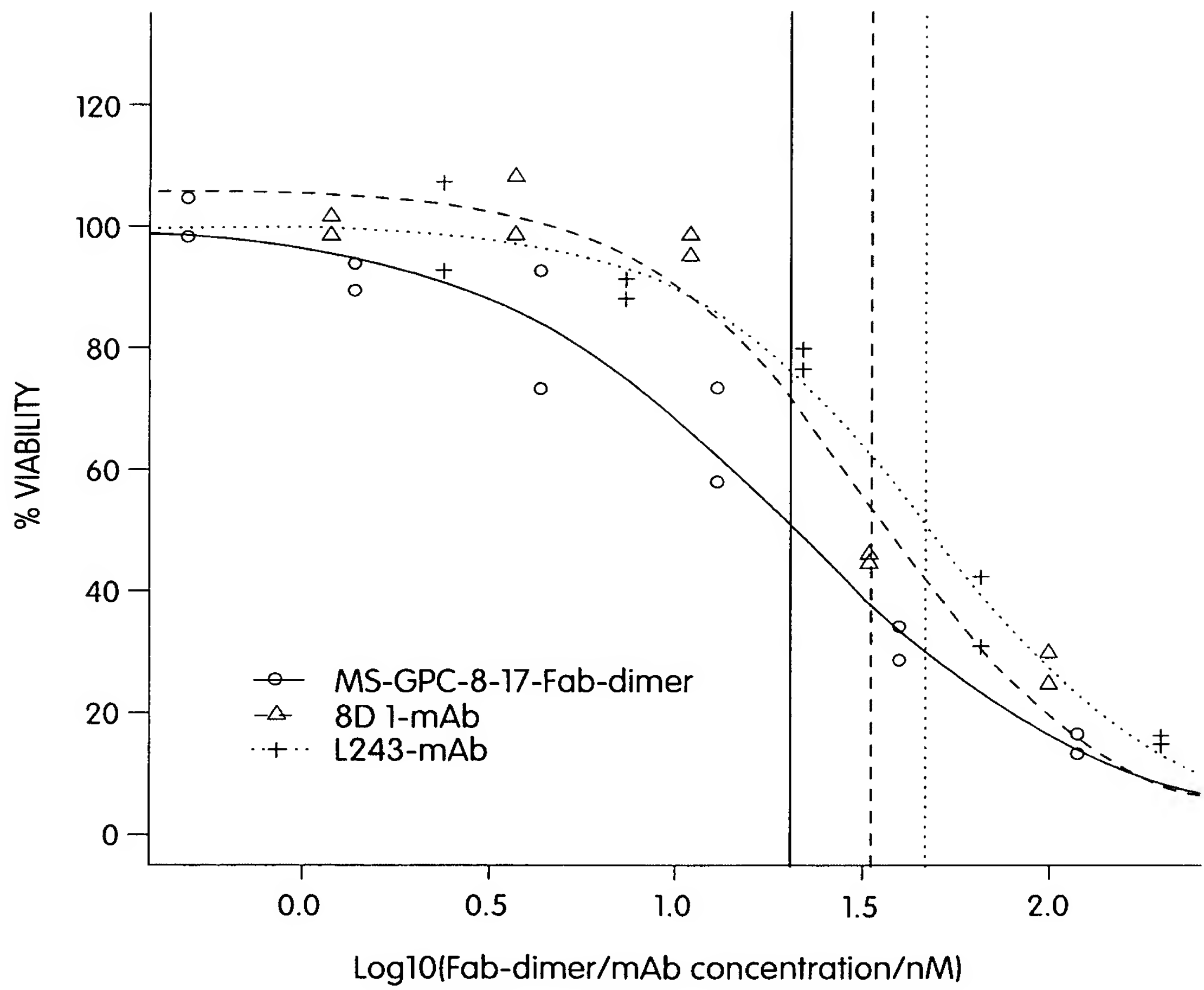


Fig. 7B

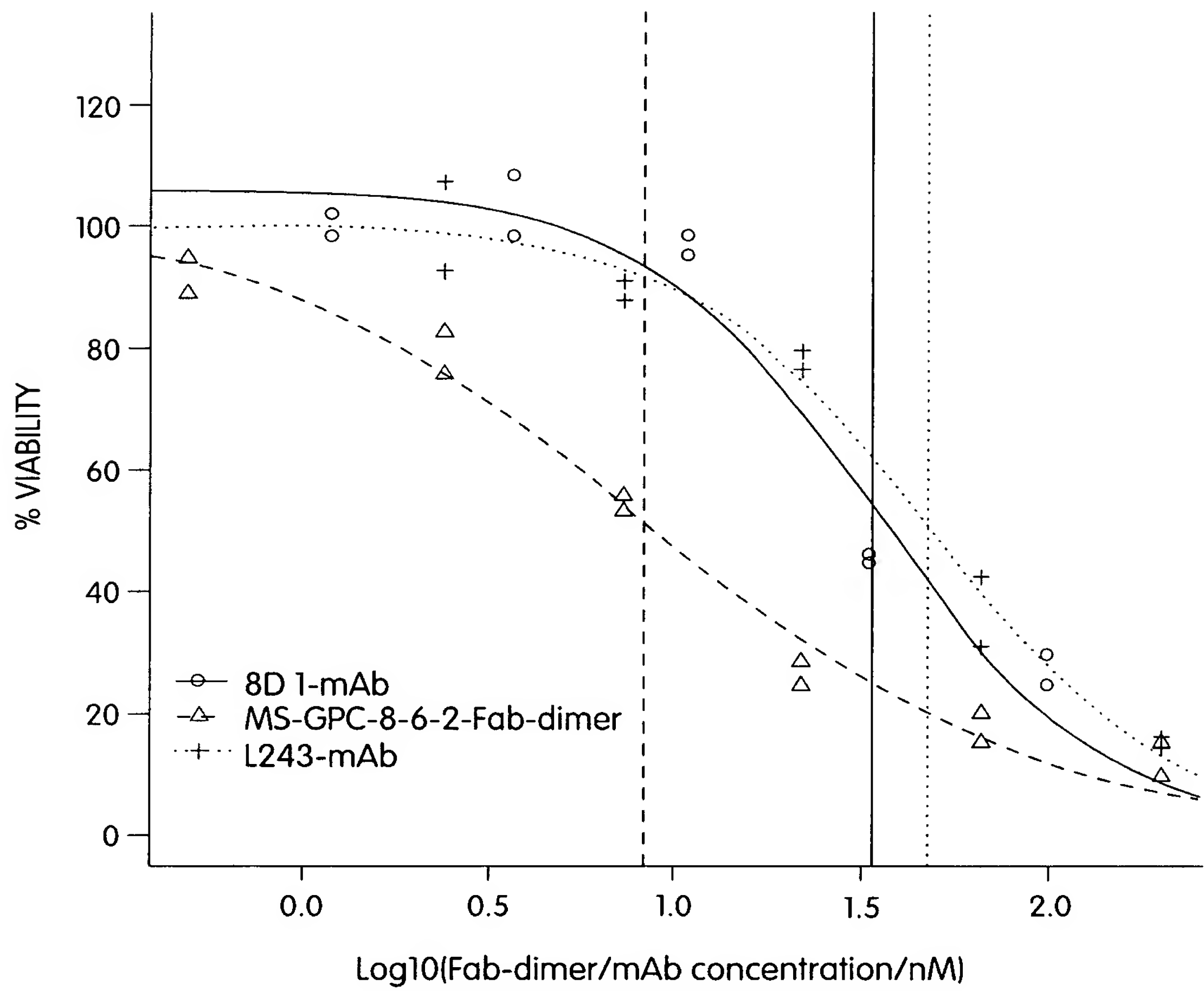


Fig. 7C

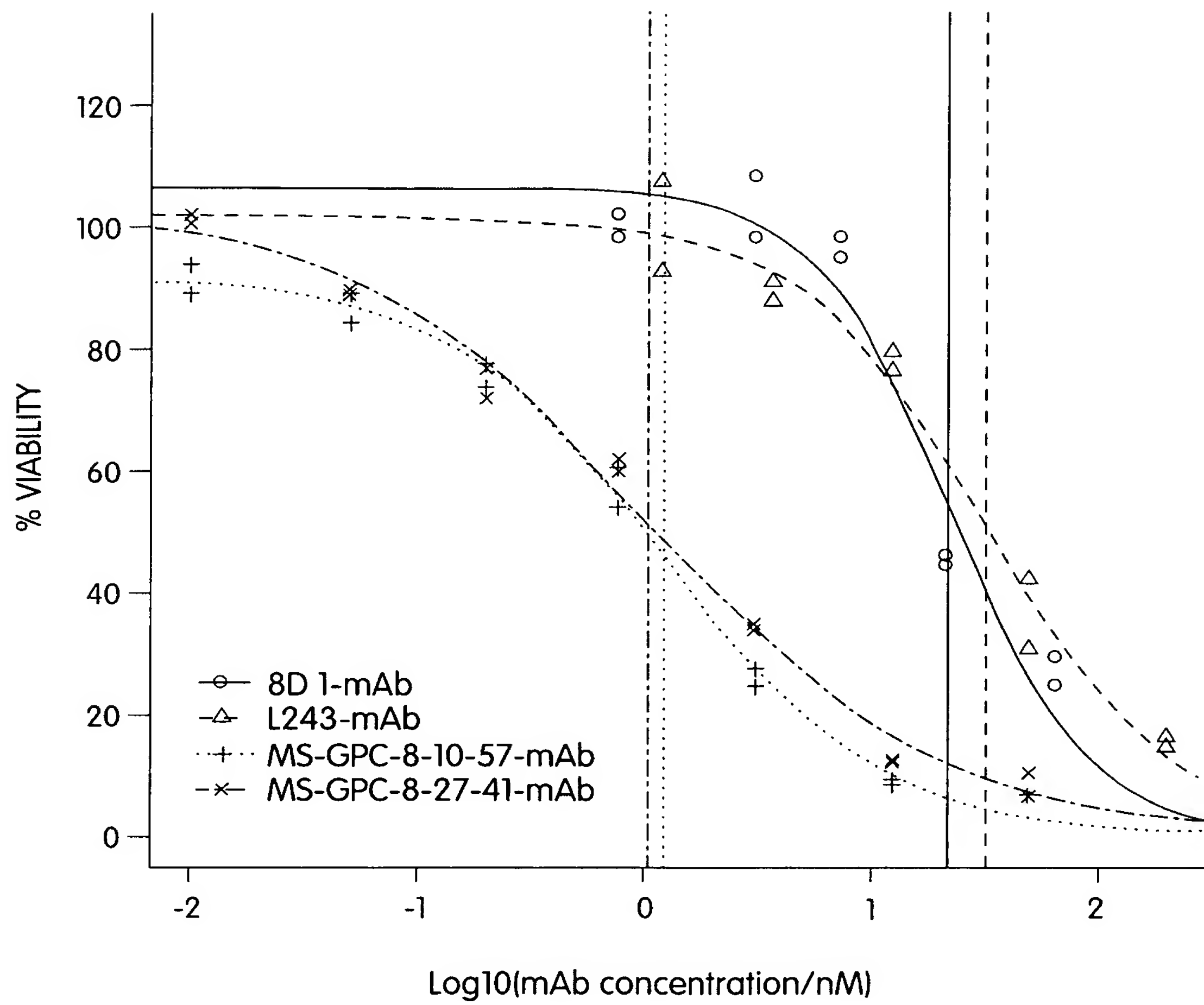


Fig. 7D

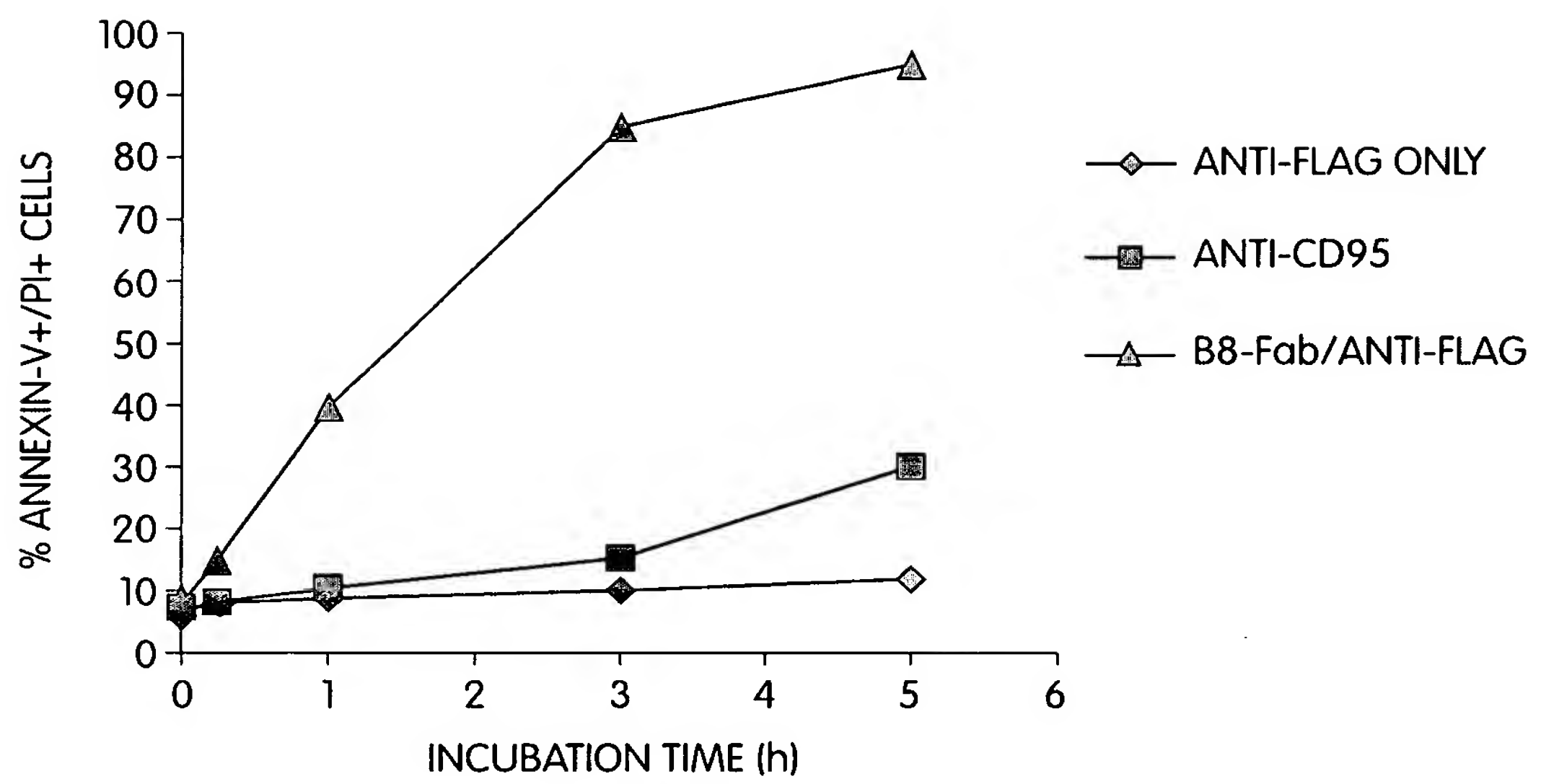


Fig. 8A

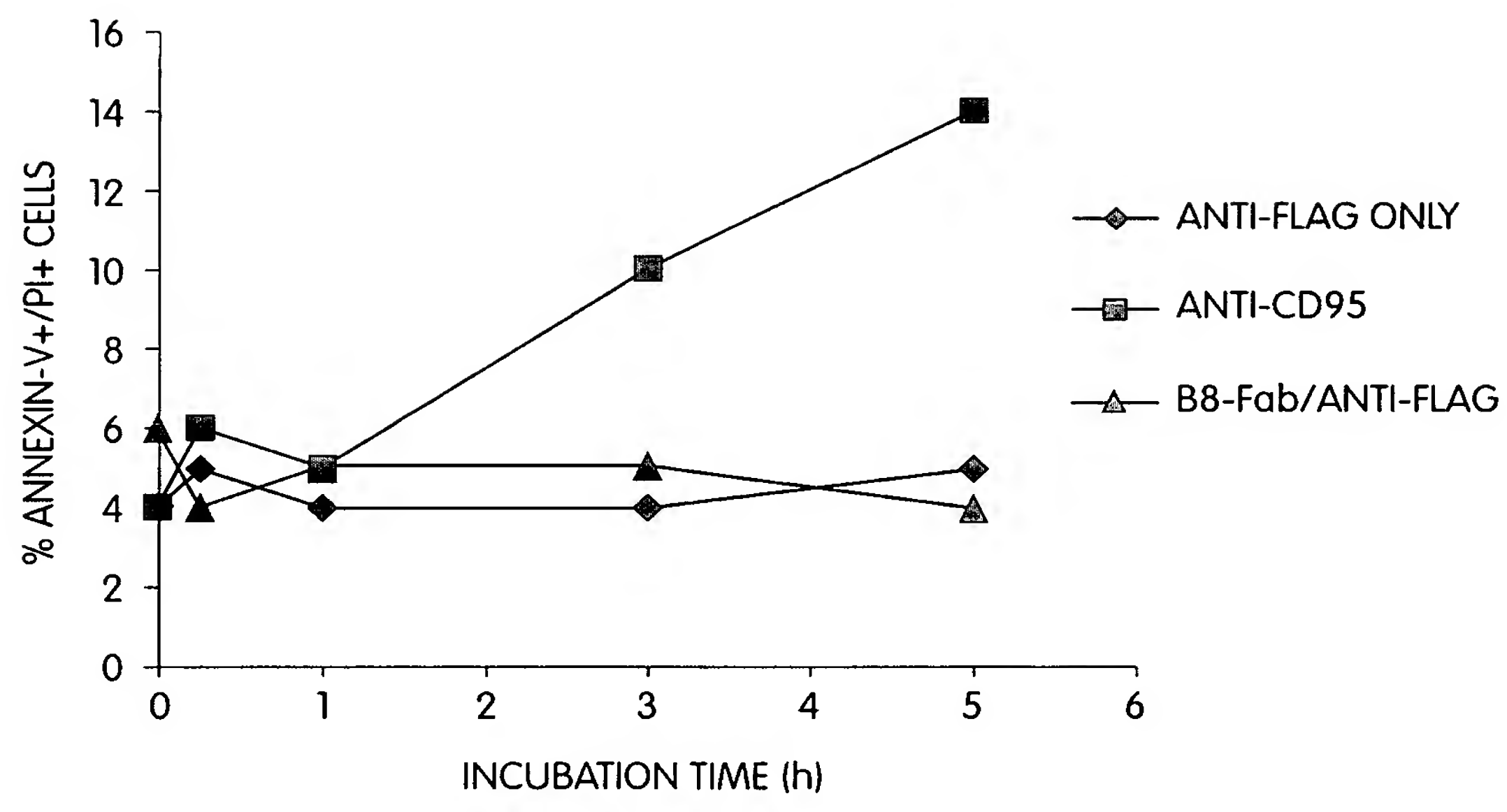


Fig. 8B



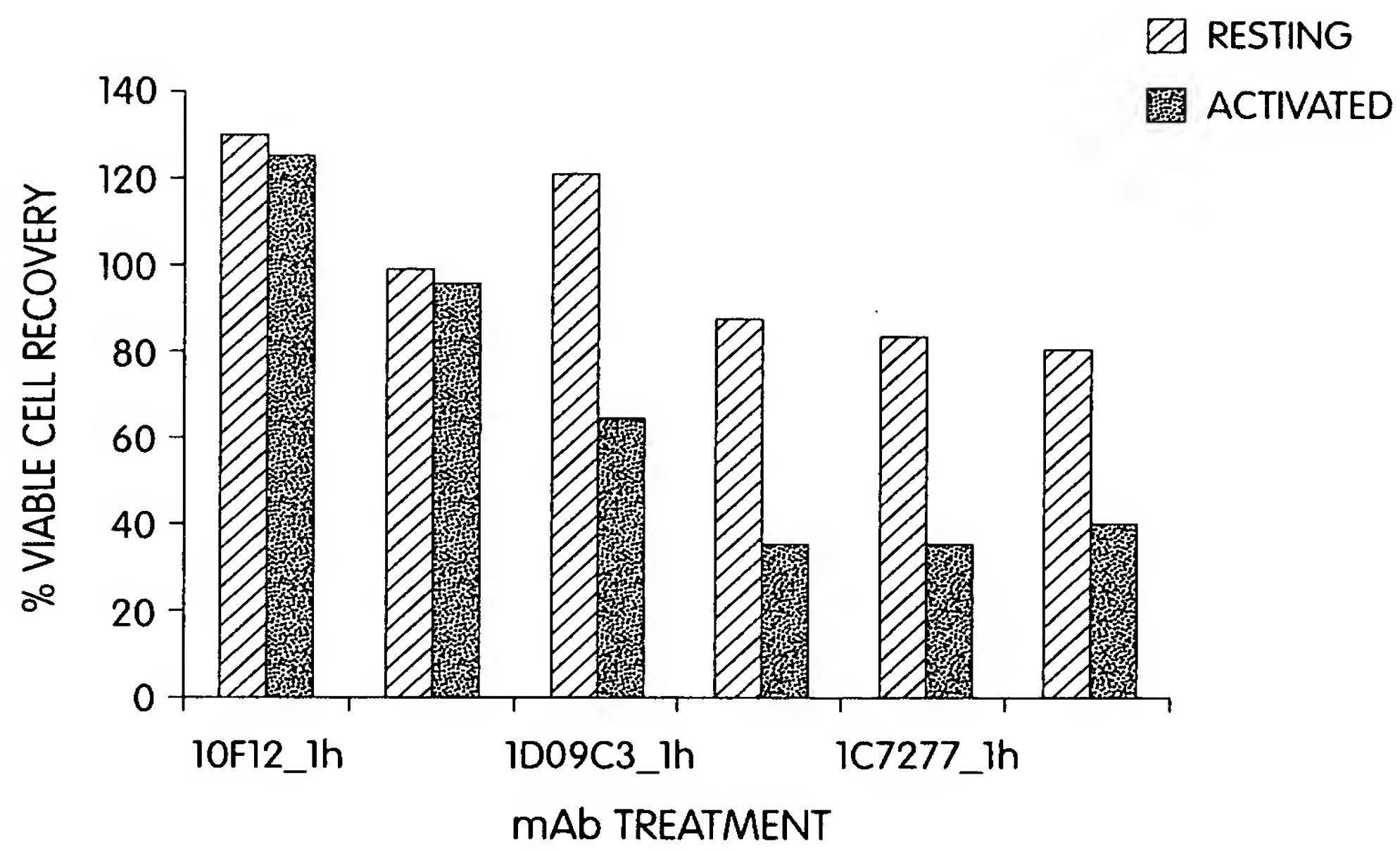


Fig. 8C

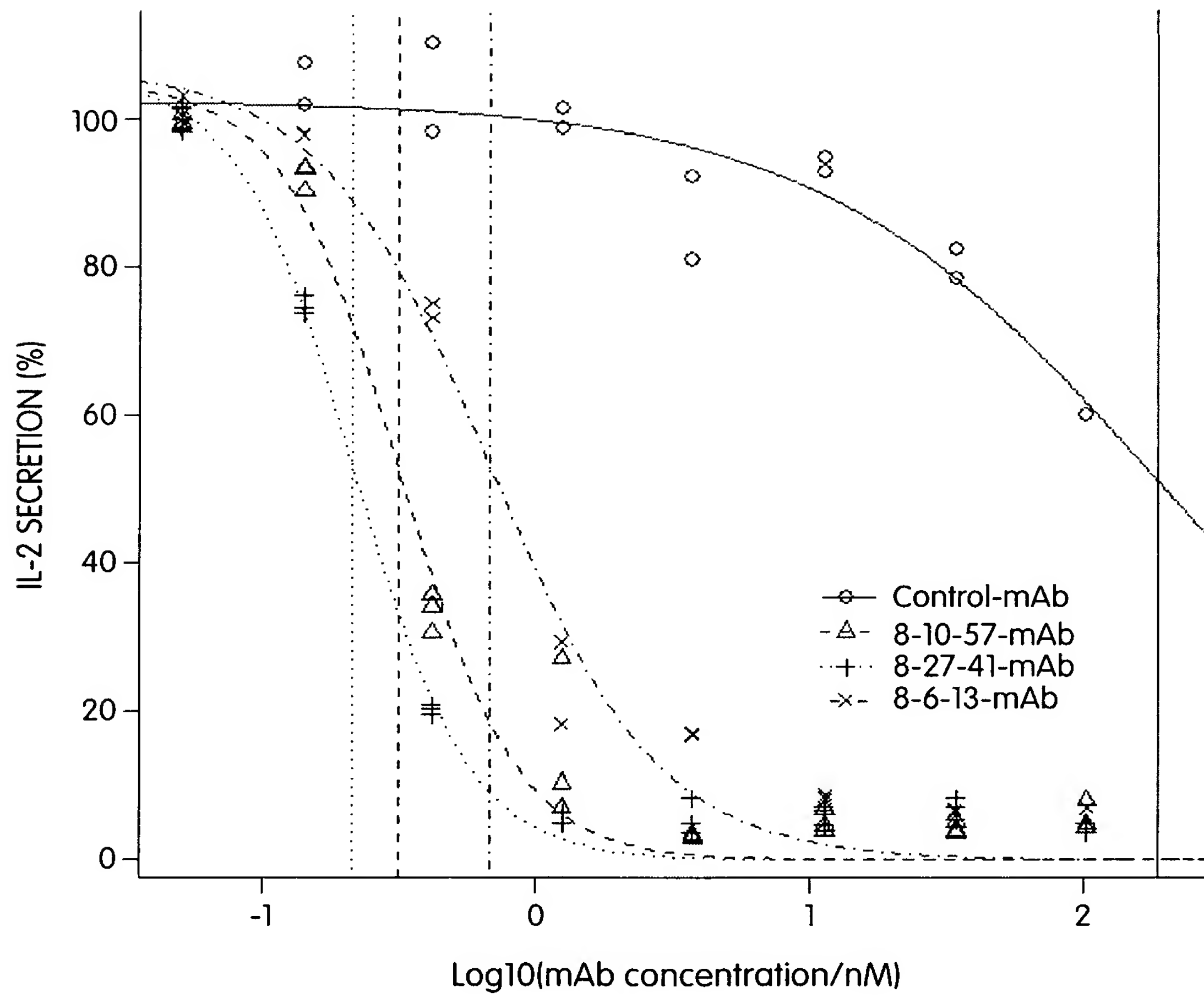


Fig. 9A

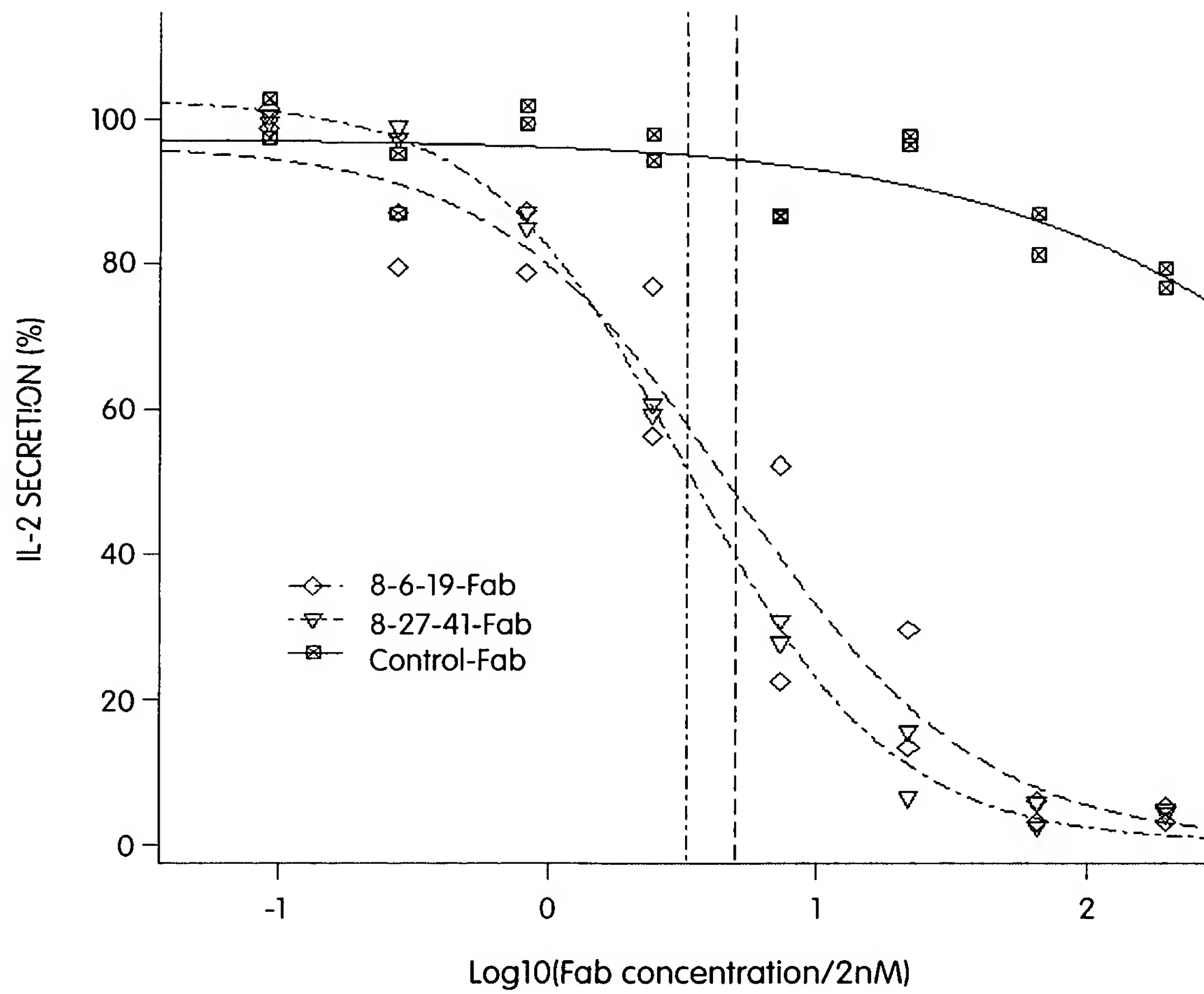


Fig. 9B

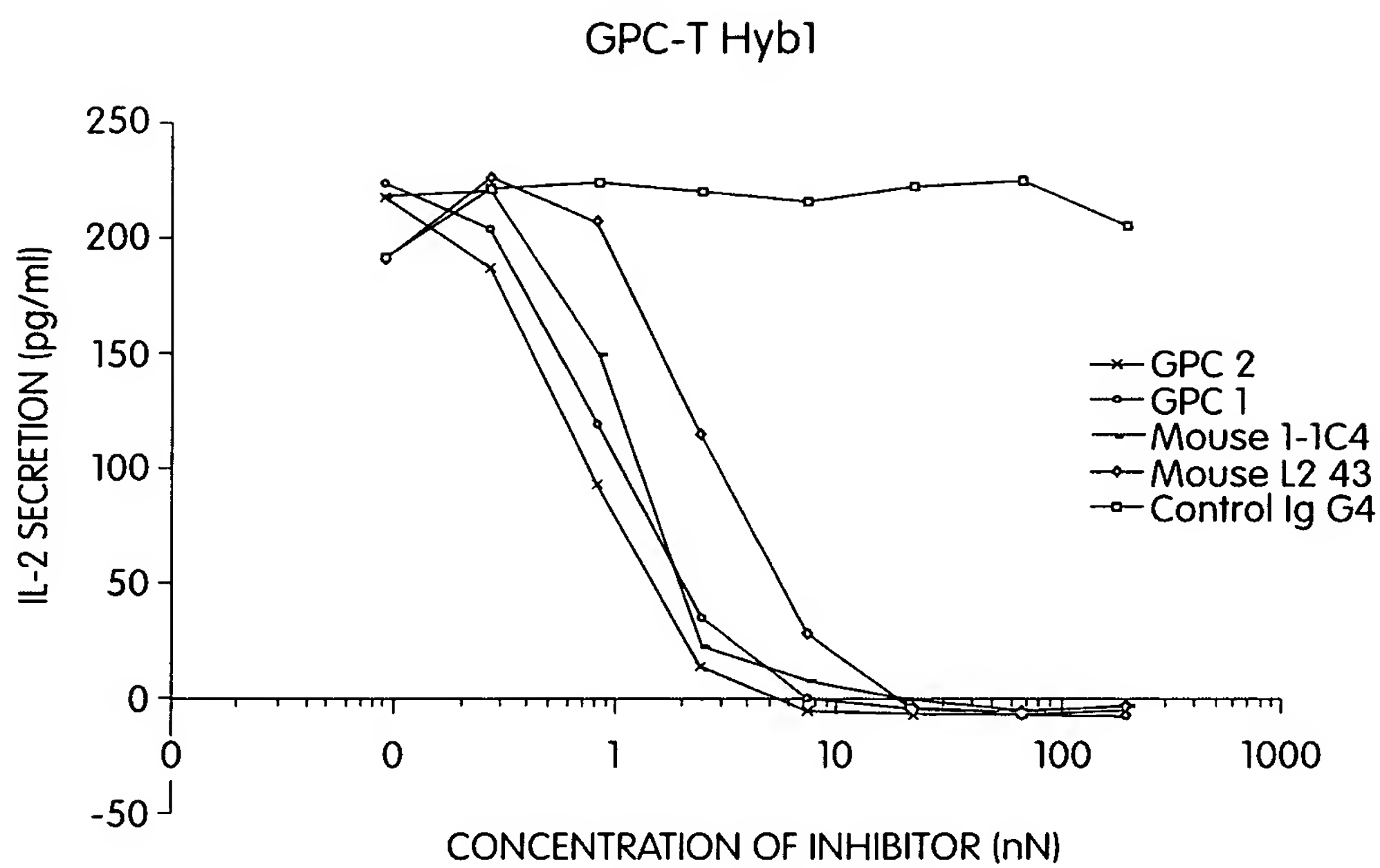


Fig. 9C

Cell line NG-TcL HA-10

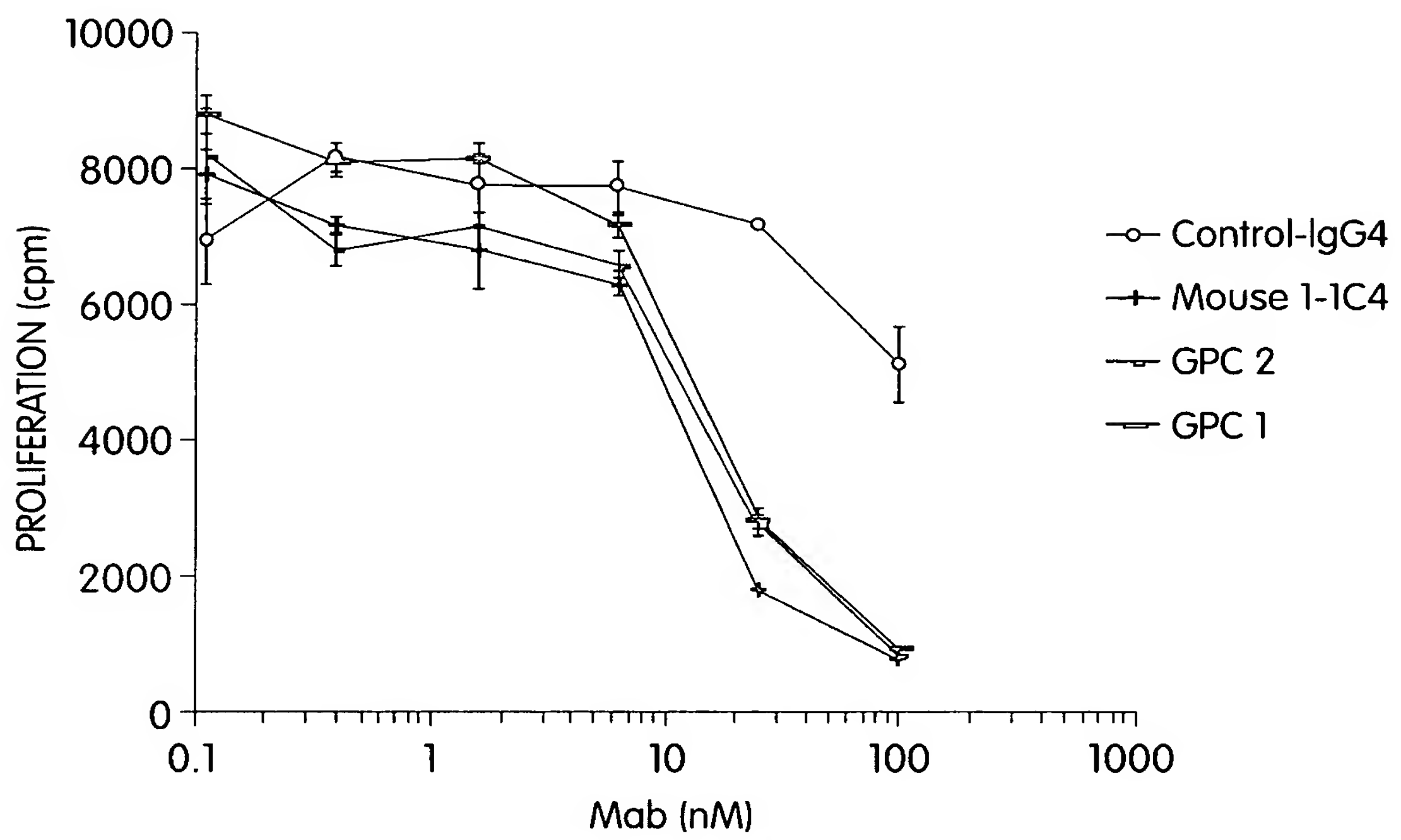


Fig. 9D

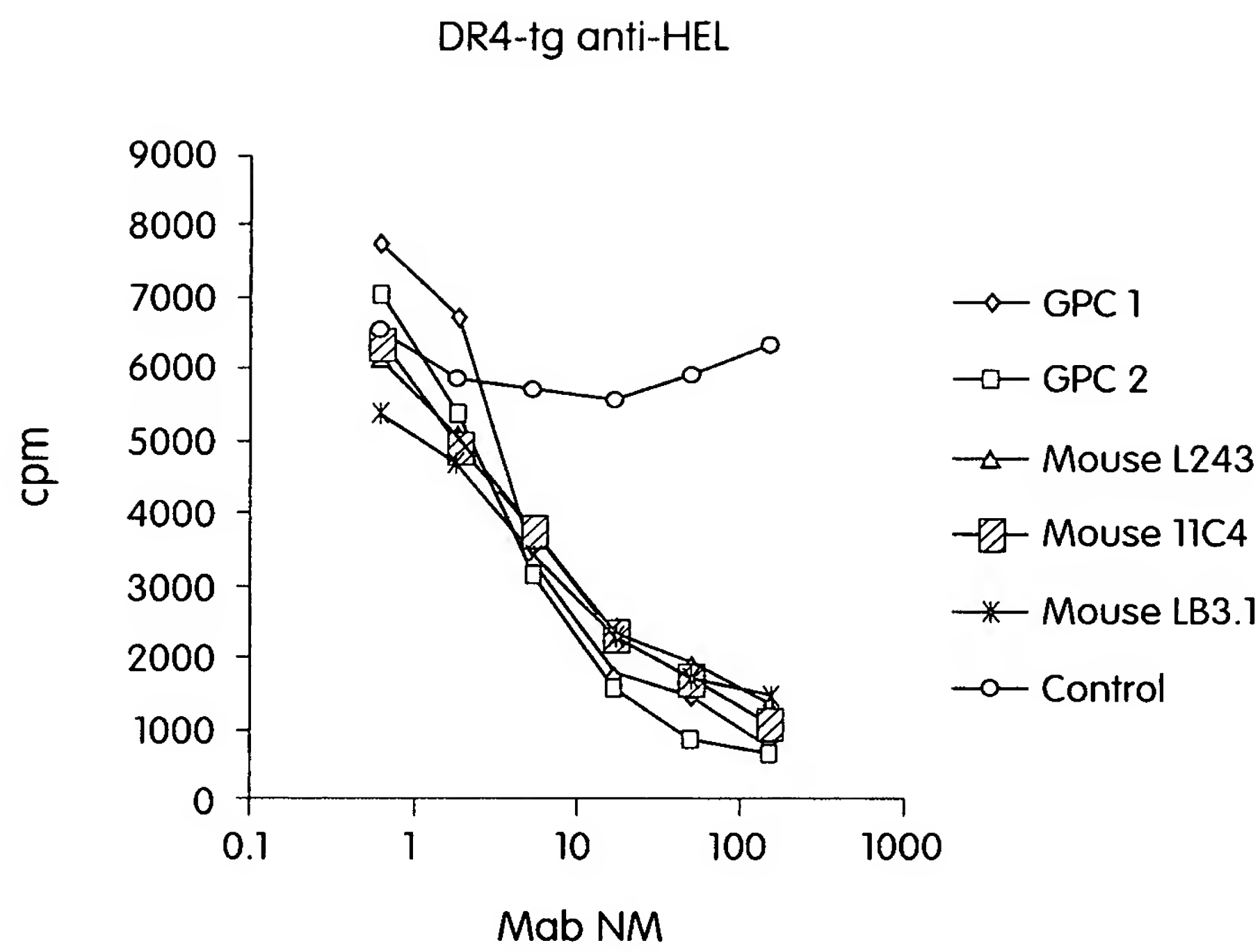


Fig. 9E

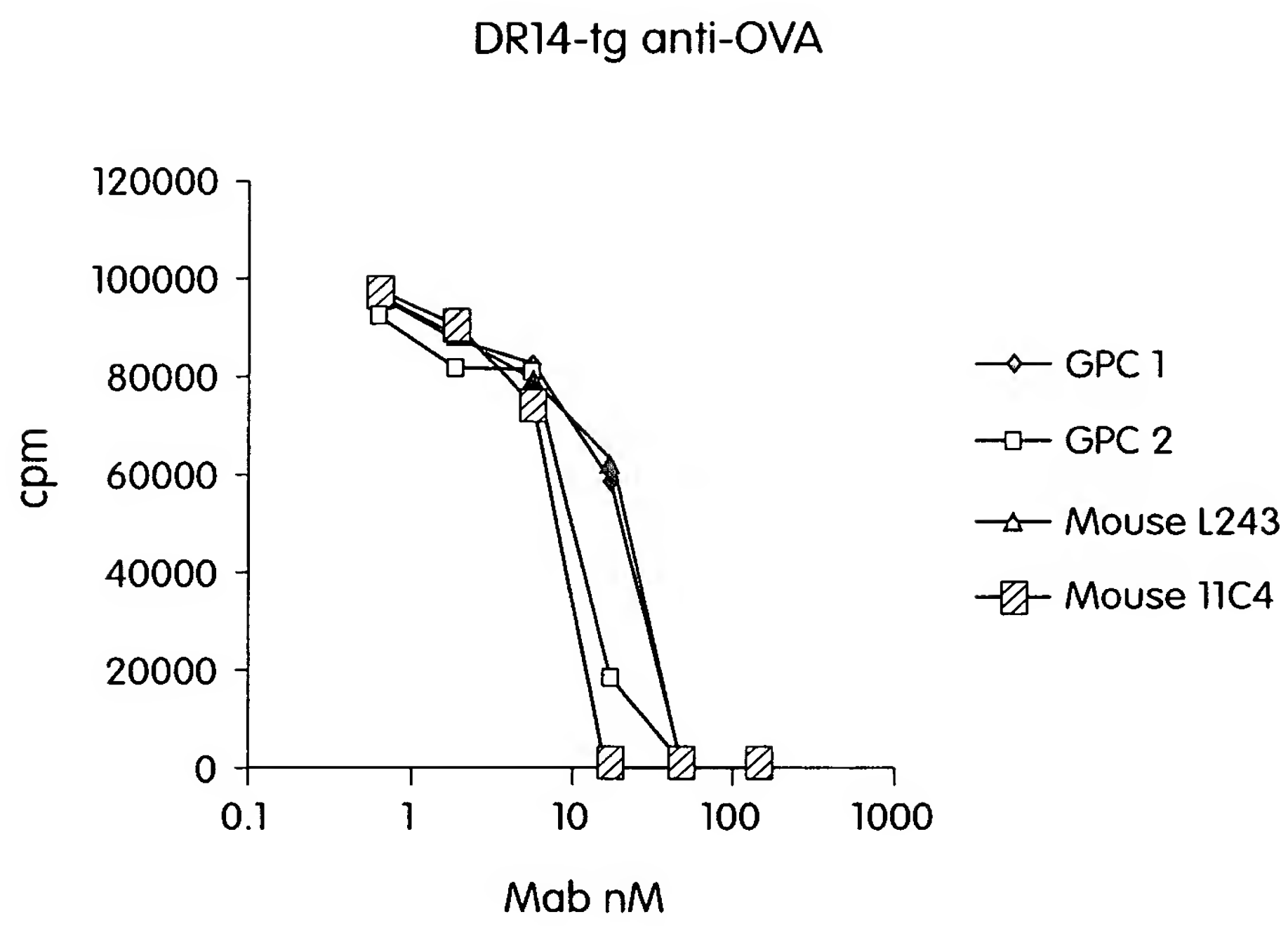


Fig. 9F

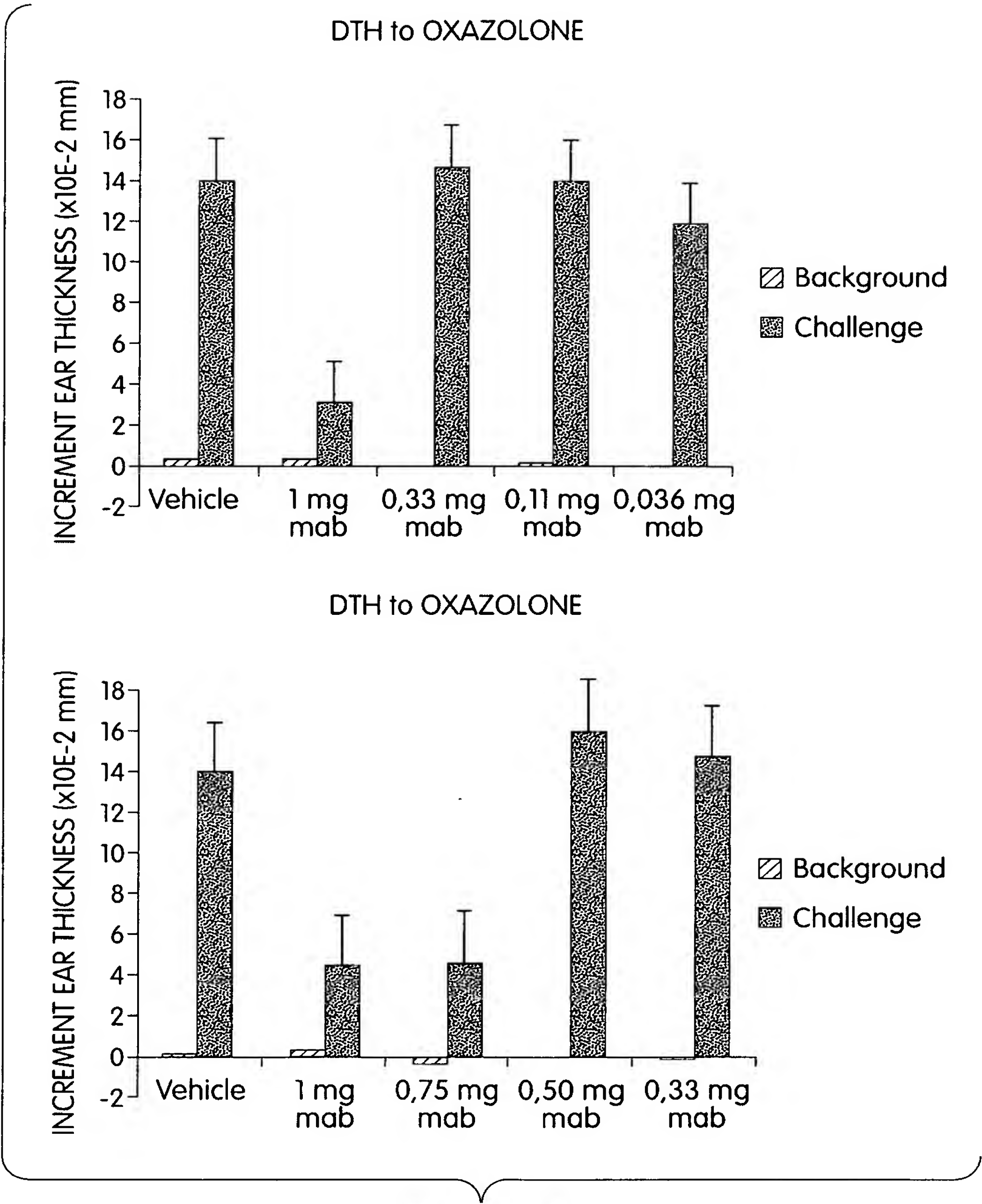


Fig. 9G



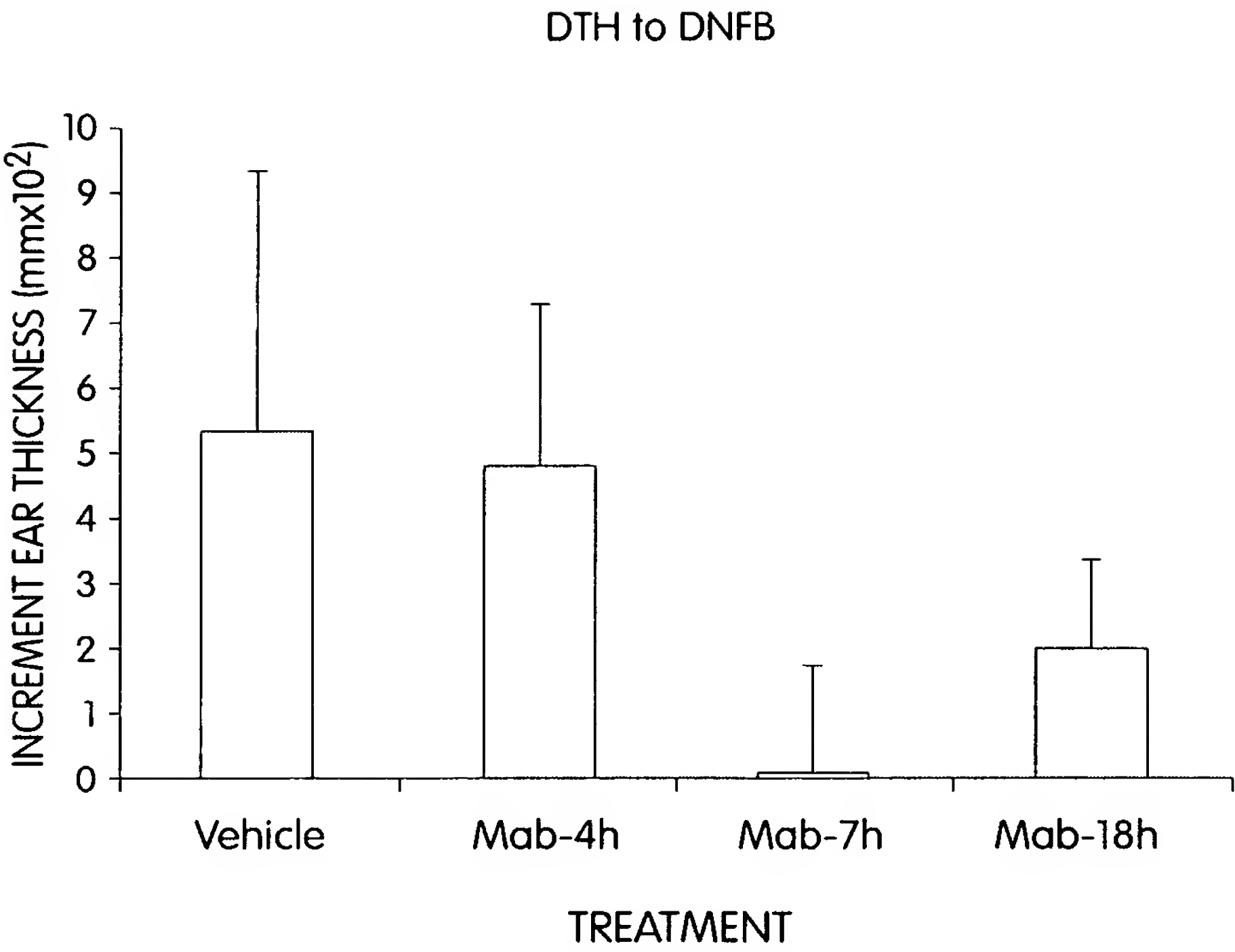


Fig. 9H

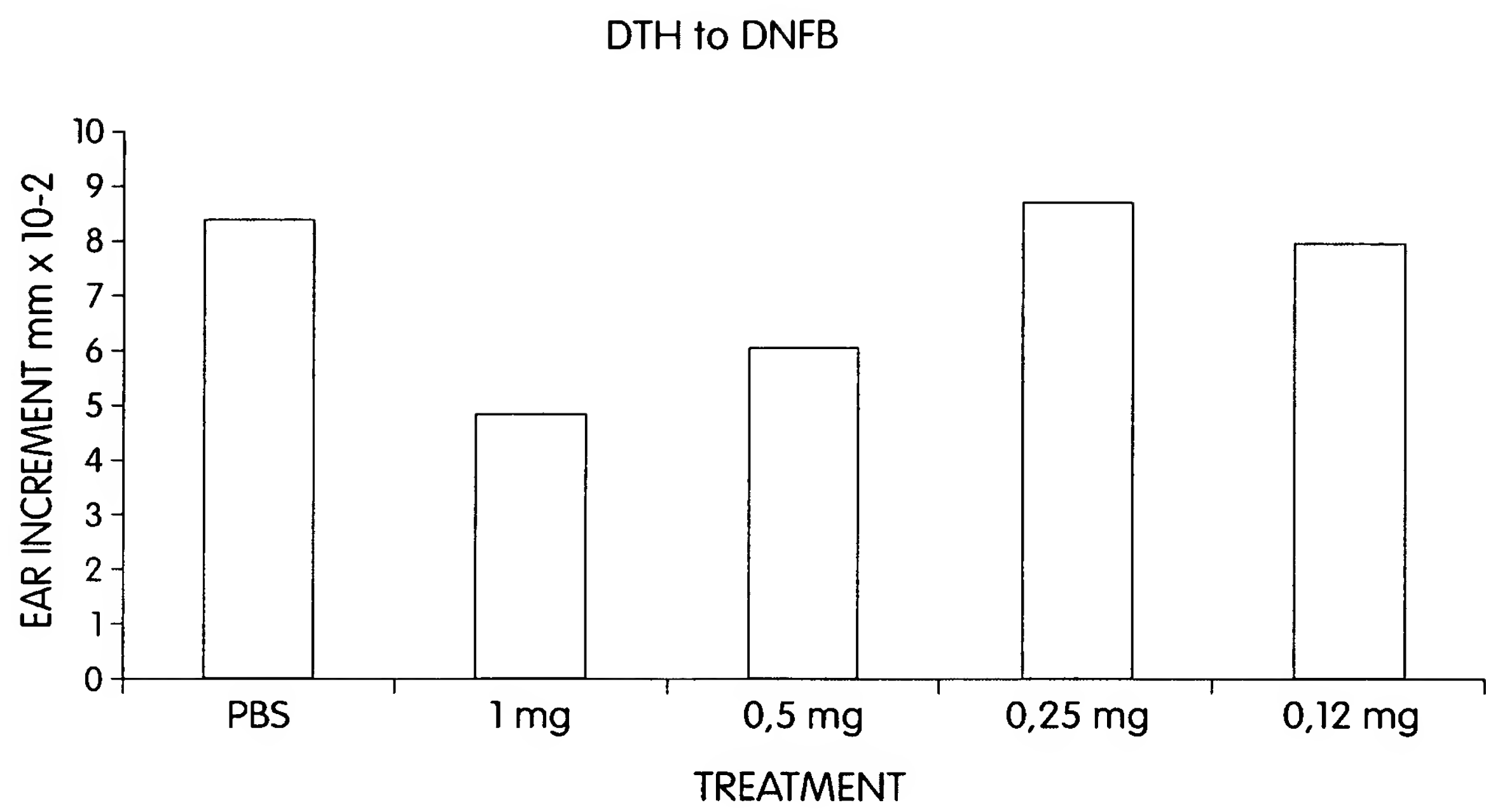


Fig. 9I

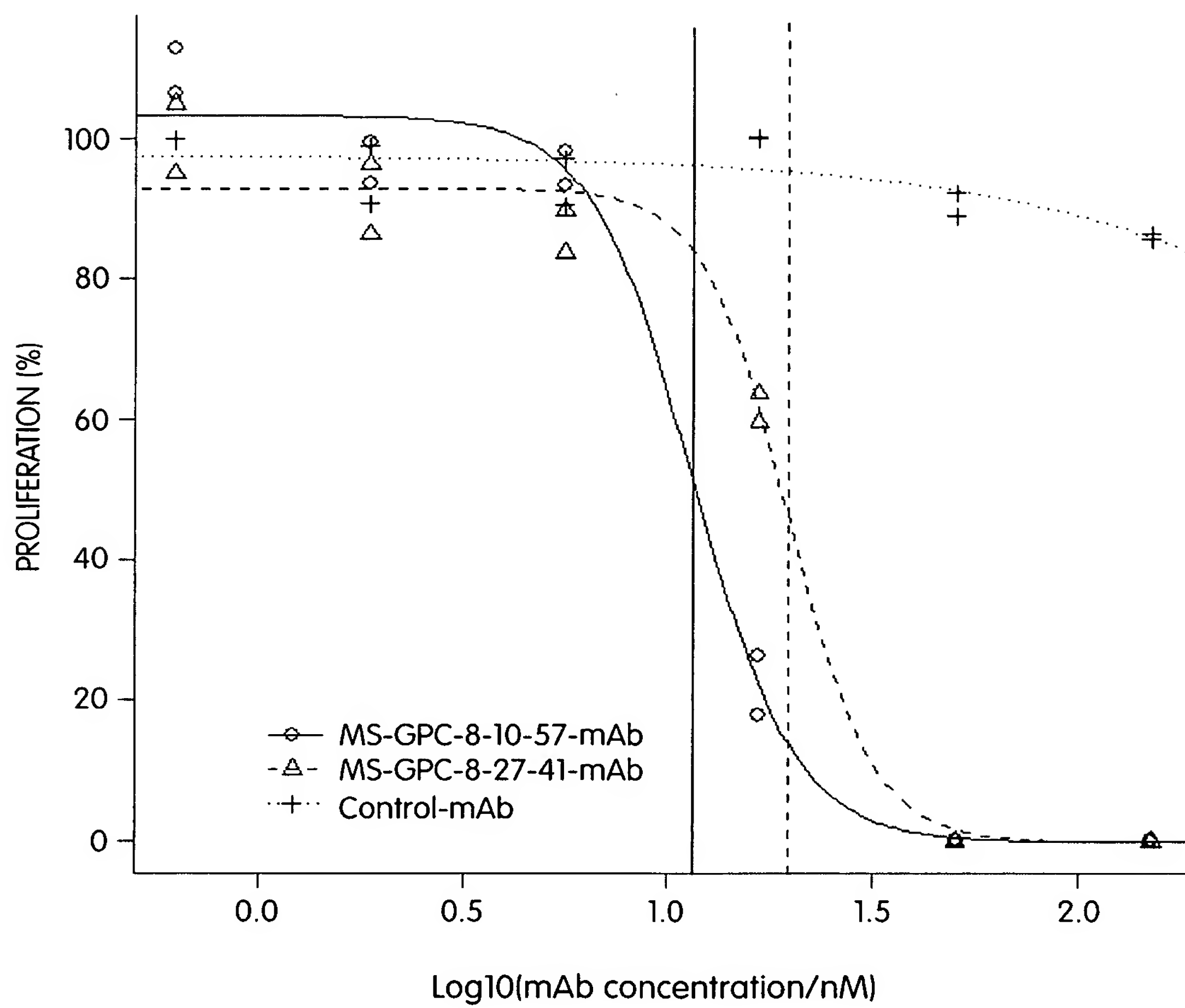


Fig. 10

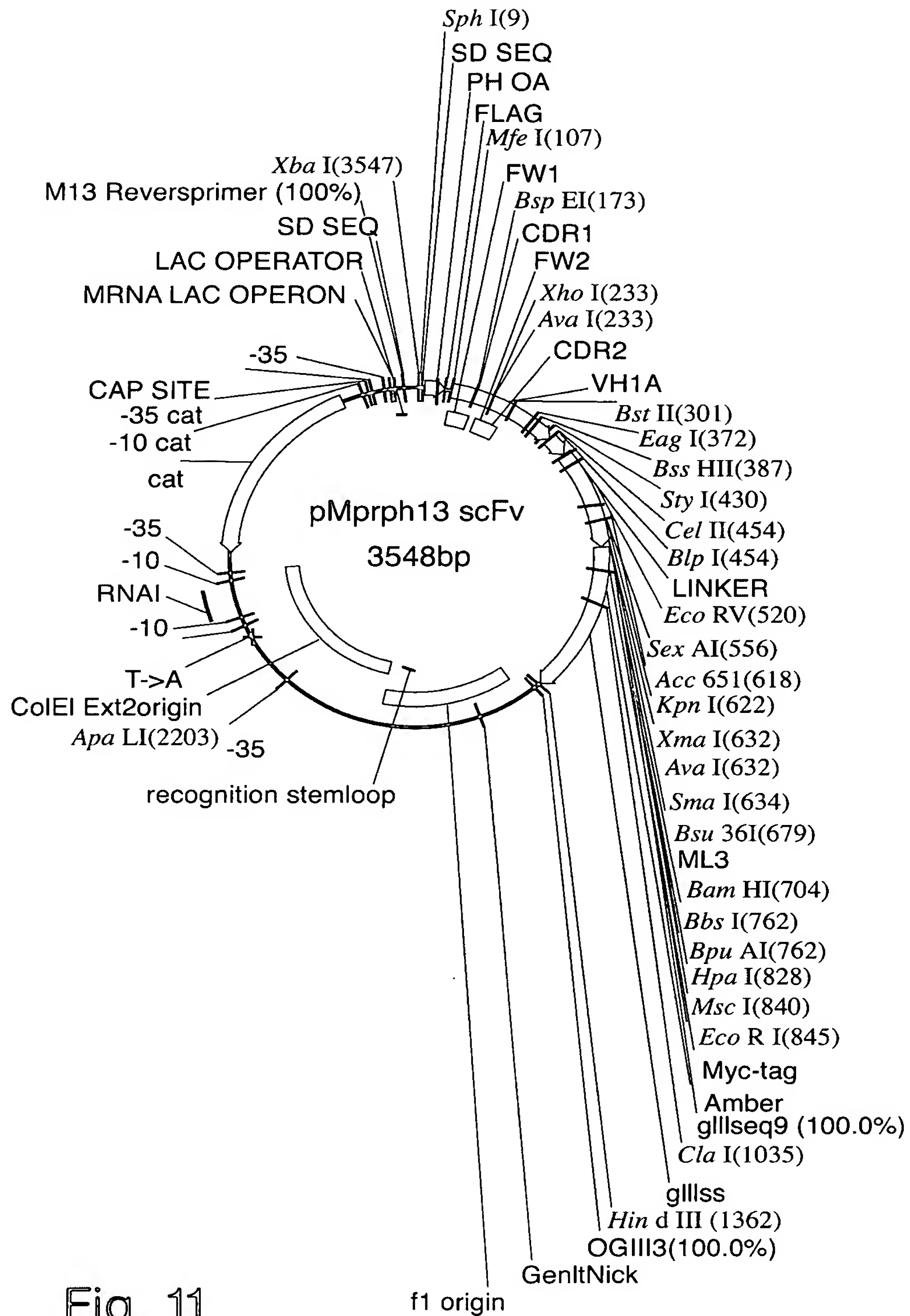


Fig. 11

XbaISphI  
 ~~~~~~  
 1 AGAGCATGCG TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC  
 TCTCGTACGC ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG  
 51 ACTCTTACCG TTGCTCTTCA CCCCTGTTAC CAAAGCCGAC TACAAAGATG  
 TGAGAATGGC AACGAGAAGT GGGGACAATG GTTTCGGCTG ATGTTTCTAC  
 MfeI  
 ~~~~~~  
 101 AAGTGCAATT GGTTCAGTCT GGCGCGGAAG TGAAAAAACC GGGCAGCAGC  
 TTCACGTAA CCAAGTCAGA CCGCGCCTTC ACTTTTTTGG CCCGTCGTCG  
 BspEI  
 ~~~~~~  
 151 GTGAAAGTGA GCTGCAAAGC CTCCGGAGGC ACTTTTAGCA GCTATGCGAT  
 CACTTTCACT CGACGTTTCG GAGGCCTCCG TGAAAATCGT CGATACGCTA  
 XhoI  
 ~~~~~~  
 AvaI  
 ~~~~~~  
 201 TAGCTGGGTG CGCCAAGCCC CTGGGCAGGG TCTCGAGTGG ATGGGCGGCA  
 ATCGACCCAC GCGGTTCGGG GACCCGTCCC AGAGCTCACC TACCCGCCGT  
 BstEII  
 ~~~~~~  
 251 TTATTCCGAT TTTTGGCACG GCGAACTACG CGCAGAAGTT TCAGGGCCGG  
 AATAAGGCTA AAAACCGTGC CGCTTGATGC GCGTCTTCAA AGTCCCGGCC  
 BstEII  
 ~~~~~~  
 301 GTGACCATTA CCGCGGATGA AAGCACCAGC ACCGCGTATA TGGAAGTGA  
 CACTGGTAAT GGCGCCTACT TTCGTGGTCG TGGCGCATAT ACCTTGACTC  
 EagI BssHII  
 ~~~~~~  
 351 CAGCCTGCGT AGCGAAGATA CGGCCGTGTA TTATTGCGCG CGTTATTATG  
 GTCGGACGCA TCGCTTCTAT GCCGGCACAT AATAACGCGC GCAATAATAC  
 StyI  
 ~~~~~~  
 401 ATCGTATGTA TAATATGGAT TATTGGGGCC AAGGCACCCT GGTGACGGTT  
 TAGCATA CAT ATTATACCTA ATAACCCCGG TTCCGTGGGA CCACTGCCAA  
 BlnI  
 ~~~~~~  
 CelII  
 ~~~~~~  
 451 AGCTCAGCGG GTGGCGGTTC TGGCGGCGGT GGGAGCGGTG GCGGTGGTTC

Fig. 11 (cont.)

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TCGAGTCGCC CACCGCCAAG ACCGCCGCCA CCTCGCCAC CGCCACCAAG

      EcoRV
      ~~~~~~
501  TGGCGGTGGT GGTTCGGATA TCGAACTGAC CCAGCCGCCT TCAGTGAGCG
      ACCGCCACCA CCAAGGCTAT AGCTTGACTG GGTCGGCGGA AGTCACTCGC

      SexAI
      ~~~~~~
551  TTGCACCAGG TCAGACCGCG CGTATCTCGT GTAGCGGCGA TGCCTGTTGC
      AACGTGGTCC AGTCTGGCGC GCATAGAGCA CATCGCCGCT ACGCGACCCG

      KpnI
      ~~~~~~
      Acc65I
      ~~~~~~
601  GATAAATACG CGAGCTGGTA CCAGCAGAAA CCCGGGCAGG CGCCAGTTCT
      CTATTTATGC GCTCGACCAT GGTCGTCTTT GGGCCCGTCC GCGGTCAAGA

      Bsu36I
      ~~~~~~
651  GGTGATTTAT GATGATTCTG ACCGTCCCTC AGGCATCCCG GAACGCTTTA
      CCACTAAATA CTACTAAGAC TGGCAGGGAG TCCGTAGGGC CTTGCGAAAT

      BamHI
      ~~~~~~
701  GCGGATCCAA CAGCGGCAAC ACCGCGACCC TGACCATTAG CGGCACTCAG
      CGCCTAGGTT GTCGCCGTTG TGGCGCTGGG ACTGGTAATC GCCGTGAGTC

      BpuAI
      ~~~~~~
      BbsI
      ~~~~~~
751  GCGGAAGACG AAGCGGATTA TTATTGCCAG AGCTATGACG CTCATATGCG
      CGCCTTCTGC TTCGCCTAAT AATAACGGTC TCGATACTGC GAGTATACGC

      HpaI
      ~~~~~~
      MscI
      ~~~~~~
      EcoRI
      ~~~~~~
801  TCCTGTGTTT GCGGGCGGCA CGAAGTTAAC CGTTCTTGGC CAGGAATTCG
      AGGACACAAA CCGCCGCCGT GCTTCAATTG GCAAGAACCG GTCCTTAAGC

851  AGCAGAAGCT GATCTCTGAG GAGGATCTGA ACTAGGGTGG TGGCTCTGGT
      TCGTCTTCGA CTAGAGACTC CTCCTAGACT TGATCCCACC ACCGAGACCA

901  TCCGGTGATT TTGATTATGA AAAGATGGCA AACGCTAATA AGGGGGCTAT
      AGGCCACTAA AACTAATACT TTTCTACCGT TTGCGATTAT TCCCCCGATA

      gIIIseq9 100.0%
      =====
951  GACCGAAAAT GCCGATGAAA ACGCGCTACA GTCTGACGCT AAAGGCAAAC

```

Fig. 11 (cont.)

|      |             |            |             |             |             |
|------|-------------|------------|-------------|-------------|-------------|
|      | CTGGCTTTTA  | CGGCTACTTT | TGCGCGATGT  | CAGACTGCGA  | TTTCCGTTTG  |
|      |             |            |             | Clal        |             |
|      |             |            |             | ~~~~~       |             |
| 1001 | TTGATTCTGT  | CGCTACTGAT | TACGGTGCTG  | CTATCGATGG  | TTTCATTGGT  |
|      | AACTAAGACA  | GCGATGACTA | ATGCCACGAC  | GATAGCTACC  | AAAGTAACCA  |
| 1051 | GACGTTTCCG  | GCCTTGCTAA | TGGTAATGGT  | GCTACTGGTG  | ATTTTGCTGG  |
|      | CTGCAAAGGC  | CGGAACGATT | ACCATTACCA  | CGATGACCAC  | TAAAACGACC  |
| 1101 | CTCTAATTCC  | CAAATGGCTC | AAGTCGGTGA  | CGGTGATAAT  | TCACCTTTAA  |
|      | GAGATTAAGG  | GTTTACCGAG | TTCAGCCACT  | GCCACTATTA  | AGTGGA AATT |
| 1151 | TGAATAATTT  | CCGTCAATAT | TTACCTTCCC  | TCCCTCAATC  | GGTTGAATGT  |
|      | ACTTATTAAA  | GGCAGTTATA | AATGGAAGGG  | AGGGAGTTAG  | CCAACTTACA  |
| 1201 | CGCCCTTTTG  | TCTTTGGCGC | TGGTAAACCA  | TATGAATTTT  | CTATTGATTG  |
|      | GCGGGAAAAC  | AGAAACCGCG | ACCATTTTGGT | ATACTTAAAA  | GATAACTAAC  |
| 1251 | TGACAAAATA  | AACTTATTCC | GTGGTGTCTT  | TGCGTTTCTT  | TTATATGTTG  |
|      | ACTGTTTTAT  | TTGAATAAGG | CACCACAGAA  | ACGCAAAGAA  | AATATACAAC  |
| 1301 | CCACCTTTAT  | GTATGTATTT | TCTACGTTTG  | CTAACATACT  | GCGTAATAAG  |
|      | GGTGGAATA   | CATACATAAA | AGATGCAAAC  | GATTGTATGA  | CGCATTATTC  |
|      |             | HindIII    |             |             |             |
|      |             | ~~~~~      |             |             |             |
| 1351 | GAGTCTTGAT  | AAGCTTGACC | TGTGAAGTGA  | AAAATGGCGC  | AGATTGTGCG  |
|      | CTCAGAACTA  | TTCGAACTGG | ACACTTCACT  | TTTTACCGCG  | TCTAACACGC  |
|      |             | OGIII3     | 100.0%      |             |             |
|      |             | =====      |             |             |             |
| 1401 | ACATTTTTTTT | TGTCTGCCGT | TTAATGAAAT  | TGTAAACGTT  | AATATTTTTGT |
|      | TGTAAAAAAA  | ACAGACGGCA | AATTACTTTA  | ACATTTGCAA  | TTATAAAACA  |
| 1451 | TAAAATTCGC  | GTTAAATTTT | TGTTAAATCA  | GCTCATTTTTT | TAACCAATAG  |
|      | ATTTTAAGCG  | CAATTTAAAA | ACAATTTAGT  | CGAGTAAAAA  | ATTGGTTATC  |
| 1501 | GCCGAAATCG  | GCAAAATCCC | TTATAAATCA  | AAAGAATAGA  | CCGAGATAGG  |
|      | CGGCTTTAGC  | CGTTTTAGGG | AATATTTAGT  | TTTCTTATCT  | GGCTCTATCC  |
| 1551 | GTTGAGTGTT  | GTTCCAGTTT | GGAACAAGAG  | TCCACTATTA  | AAGAACGTGG  |
|      | CAACTCACAA  | CAAGGTCAAA | CCTTGTTCTC  | AGGTGATAAT  | TTCTTGCACC  |
| 1601 | ACTCCAACGT  | CAAAGGGCGA | AAAACCGTCT  | ATCAGGGCGA  | TGGCCCACTA  |
|      | TGAGGTTGCA  | GTTTCCCGCT | TTTTGGCAGA  | TAGTCCCGCT  | ACCGGGTGAT  |
| 1651 | CGAGAACCAT  | CACCCTAATC | AAGTTTTTTTG | GGGTCGAGGT  | GCCGTAAAGC  |
|      | GCTCTTGGTA  | GTGGGATTAG | TTCAAAAAAC  | CCCAGCTCCA  | CGGCATTTTCG |
| 1701 | ACTAAATCGG  | AACCCTAAAG | GGAGCCCCCG  | ATTTAGAGCT  | TGACGGGGAA  |
|      | TGATTTAGCC  | TTGGGATTTT | CCTCGGGGGC  | TAAATCTCGA  | ACTGCCCTT   |

Fig. 11 (cont.)

|      |                                                    |                          |                          |                          |                          |
|------|----------------------------------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 1751 | AGCCGGCGAA<br>TCGGCCGCTT                           | CGTGGCGAGA<br>GCACCGCTCT | AAGGAAGGGA<br>TTCCTTCCCT | AGAAAGCGAA<br>TCTTTCGCTT | AGGAGCGGGC<br>TCCTCGCCCC |
| 1801 | GCTAGGGCGC<br>CGATCCCGCG                           | TGGCAAGTGT<br>ACCGTTCACA | AGCGGTCACG<br>TCGCCAGTGC | CTGCGCGTAA<br>GACGCGCATT | CCACCACACC<br>GGTGGTGTGG |
| 1851 | CGCCGCGCTT<br>GCGGCGCGAA                           | AATGCGCCGC<br>TTACGCGGCG | TACAGGGCGC<br>ATGTCCCGCG | GTGCTAGCCA<br>CACGATCGGT | TGTGAGCAAA<br>ACACTCGTTT |
| 1901 | AGGCCAGCAA<br>TCCGGTCGTT                           | AAGGCCAGGA<br>TTCCGGTCCT | ACCGTAAAAA<br>TGGCATTTTT | GGCCGCGTTG<br>CCGGCGCAAC | CTGGCGTTTT<br>GACCGCAAAA |
| 1951 | TCCATAGGCT<br>AGGTATCCGA                           | CCGCCCCCCT<br>GGCGGGGGGA | GACGAGCATC<br>CTGCTCGTAG | ACAAAAATCG<br>TGTTTTTAGC | ACGCTCAAGT<br>TGCGAGTTCA |
| 2001 | CAGAGGTGGC<br>GTCTCCACCG                           | GAAACCCGAC<br>CTTTGGGCTG | AGGACTATAA<br>TCCTGATATT | AGATACCAGG<br>TCTATGGTCC | CGTTTCCCCC<br>GCAAAGGGGG |
| 2051 | TGGAAGCTCC<br>ACCTTCGAGG                           | CTCGTGCGCT<br>GAGCACGCGA | CTCCTGTTCC<br>GAGGACAAGG | GACCCTGCCG<br>CTGGGACGGC | CTTACCGGAT<br>GAATGGCCTA |
| 2101 | ACCTGTCCGC<br>TGGACAGGCG                           | CTTTCTCCCT<br>GAAAGAGGGA | TCGGGAAGCG<br>AGCCCTTCGC | TGGCGCTTTC<br>ACCGCGAAAG | TCATAGCTCA<br>AGTATCGAGT |
| 2151 | CGCTGTAGGT<br>GCGACATCCA                           | ATCTCAGTTC<br>TAGAGTCAAG | GGTGTAGGTC<br>CCACATCCAG | GTTGCTCCA<br>CAAGCGAGGT  | AGCTGGGCTG<br>TCGACCCGAC |
|      | <p style="text-align: center;">ApaLI<br/>~~~~~</p> |                          |                          |                          |                          |
| 2201 | TGTGCACGAA<br>ACACGTGCTT                           | CCCCCGTTT<br>GGGGGGCAAG  | AGTCCGACCG<br>TCAGGCTGGC | CTGCGCCTTA<br>GACGCGGAAT | TCCGGTAACT<br>AGGCCATTGA |
| 2251 | ATCGTCTTGA<br>TAGCAGAACT                           | GTCCAACCCG<br>CAGGTTGGGC | GTAAGACACG<br>CATTCTGTGC | ACTTATCGCC<br>TGAATAGCGG | ACTGGCAGCA<br>TGACCGTCGT |
| 2301 | GCCACTGGTA<br>CGGTGACCAT                           | ACAGGATTAG<br>TGTCTTAATC | CAGAGCGAGG<br>GTCTCGCTCC | TATGTAGGCG<br>ATACATCCGC | GTGCTACAGA<br>CACGATGTCT |
| 2351 | GTTCTTGAAG<br>CAAGAACTTC                           | TGGTGGCCTA<br>ACCACCGGAT | ACTACGGCTA<br>TGATGCCGAT | CACTAGAAGA<br>GTGATCTTCT | ACAGTATTTG<br>TGTCATAAAC |
| 2401 | GTATCTGCGC<br>CATAGACGCG                           | TCTGCTGTAG<br>AGACGACATC | CCAGTTACCT<br>GGTCAATGGA | TCGGAAAAAG<br>AGCCTTTTTT | AGTTGGTAGC<br>TCAACCATCG |
| 2451 | TCTTGATCCG<br>AGAAGTAGGC                           | GCAAACAAAC<br>CGTTTGTTTG | CACCGCTGGT<br>GTGGCGACCA | AGCGGTGGTT<br>TCGCCACCAA | TTTTTGTTTG<br>AAAAACAAAC |
| 2501 | CAAGCAGCAG<br>GTTGTCGTC                            | ATTACGCGCA<br>TAATGCGCGT | GAAAAAAGG<br>CTTTTTTTCC  | ATCTCAAGAA<br>TAGAGTTCTT | GATCCTTTGA<br>CTAGGAAACT |
| 2551 | TCTTTTCTAC                                         | GGGGTCTGAC               | GCTCAGTGGA               | ACGAAAATC                | ACGTTAAGGG               |

Fig. 11 (cont.)



|      |                           |                           |                          |                           |                          |
|------|---------------------------|---------------------------|--------------------------|---------------------------|--------------------------|
|      | AGAAAAGATG                | CCCCAGACTG                | CGAGTCACCT               | TGCTTTTGAG                | TGCAATTCCC               |
| 2601 | ATTTTGGTCA<br>TAAAACCAGT  | GATCTAGCAC<br>CTAGATCGTG  | CAGGCGTTTA<br>GTCCGCAAAT | AGGGCACCAA<br>TCCCGTGGTT  | TAAGTGCCTT<br>ATTGACGGAA |
| 2651 | AAAAAAATTA<br>TTTTTTTAAT  | CGCCCCGCCC<br>GCGGGGCGGG  | TGCCACTCAT<br>ACGGTGAGTA | CGCAGTACTG<br>GCGTCATGAC  | TTGTAATTCA<br>AACATTAAGT |
| 2701 | TTAAGCATTG<br>AATTCGTAAG  | TGCCGACATG<br>ACGGCTGTAC  | GAAGCCATCA<br>CTTCGGTAGT | CAAACGGCAT<br>GTTTGCCGTA  | GATGAACCTG<br>CTACTTGGAC |
| 2751 | AATCGCCAGC<br>TTAGCGGTCG  | GGCATCAGCA<br>CCGTAGTCGT  | CCTTGTCGCC<br>GGAACAGCGG | TTGCGTATAA<br>AACGCATATT  | TATTTGCCCA<br>ATAAACGGGT |
| 2801 | TAGTGAAAAC<br>ATCACTTTTG  | GGGGGCGAAG<br>CCCCCGCTTC  | AAGTTGTCCA<br>TTCAACAGGT | TATTGGCTAC<br>ATAACCGATG  | GTTTAAATCA<br>CAAATTTAGT |
| 2851 | AAACTGGTGA<br>TTTGACCACT  | AACTCACCCA<br>TTGAGTGGGT  | GGGATTGGCT<br>CCCTAACCGA | GAGACGAAAA<br>CTCTGCTTTT  | ACATATTCTC<br>TGTATAAGAG |
| 2901 | AATAAACCCCT<br>TTATTTGGGA | TTAGGGGAAAT<br>AATCCCTTTA | AGGCCAGGTT<br>TCCGGTCCAA | TTCACCGTAA<br>AAGTGGCATT  | CACGCCACAT<br>GTGCGGTGTA |
| 2951 | CTTGCGAATA<br>GAACGCTTAT  | TATGTGTAGA<br>ATACACATCT  | AACTGCCGGA<br>TTGACGGCCT | AATCGTCGTG<br>TTAGCAGCAC  | GTATTCCTC<br>CATAAGTGAG  |
| 3001 | CAGAGCGATG<br>GTCTCGCTAC  | AAAACGTTTC<br>TTTTGCAAAG  | AGTTTGCTCA<br>TCAAACGAGT | TGGAAAACGG<br>ACCTTTTGCC  | TGTAACAAGG<br>ACATTGTTCC |
| 3051 | GTGAACACTA<br>CACTTGTGAT  | TCCCATATCA<br>AGGGTATAGT  | CCAGCTCACC<br>GGTCGAGTGG | GTCTTTCATT<br>CAGAAAGTAA  | GCCATACGGA<br>CGGTATGCCT |
| 3101 | ACTCCGGGTG<br>TGAGGCCAC   | AGCATTCATC<br>TCGTAAAGTAG | AGGCGGGCAA<br>TCCGCCCGTT | GAATGTGAAT<br>CTTACACTTA  | AAAGGCCGGA<br>TTTCCGGCCT |
| 3151 | TAAAACTTGT<br>ATTTTGAACA  | GCTTATTTTT<br>CGAATAAAAA  | CTTTACGGTC<br>GAAATGCCAG | TTTAAAAAGG<br>AAATTTTTTCC | CCGTAATATC<br>GGCATTATAG |
| 3201 | CAGCTGAACG<br>GTCGACTTGC  | GTCTGGTTAT<br>CAGACCAATA  | AGGTACATTG<br>TCCATGTAAC | AGCAACTGAC<br>TCGTTGACTG  | TGAAATGCCT<br>ACTTTACGGA |
| 3251 | CAAAATGTTC<br>GTTTTACAAG  | TTTACGATGC<br>AAATGCTACG  | CATTGGGATA<br>GTAACCCTAT | TATCAACGGT<br>ATAGTTGCCA  | GGTATATCCA<br>CCATATAGGT |
| 3301 | GTGATTTTTT<br>CACTAAAAAA  | TCTCCATTTT<br>AGAGGTAAAA  | AGCTTCCTTA<br>TCGAAGGAAT | GCTCCTGAAA<br>CGAGGACTTT  | ATCTCGATAA<br>TAGAGCTATT |
| 3351 | CTCAAAAAAT<br>GAGTTTTTTA  | ACGCCCCGGTA<br>TGCGGGCCAT | GTGATCTTAT<br>CACTAGAATA | TTCATTATGG<br>AAGTAATACC  | TGAAAGTTGG<br>ACTTTCAACC |
| 3401 | AACCTCACCC<br>TTGGAGTGGG  | GACGTCTAAT<br>CTGCAGATTA  | GTGAGTTAGC<br>CACTCAATCG | TCACTCATTG<br>AGTGAGTAAT  | GGCACCCAG<br>CCGTGGGGTC  |

Fig. 11 (cont.)

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3451  GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG
      CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

      M13 Reverse primer 100.0% XbaI
      =====
3501  ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCT
      TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAAAGA
```

Fig. 11 (cont.)

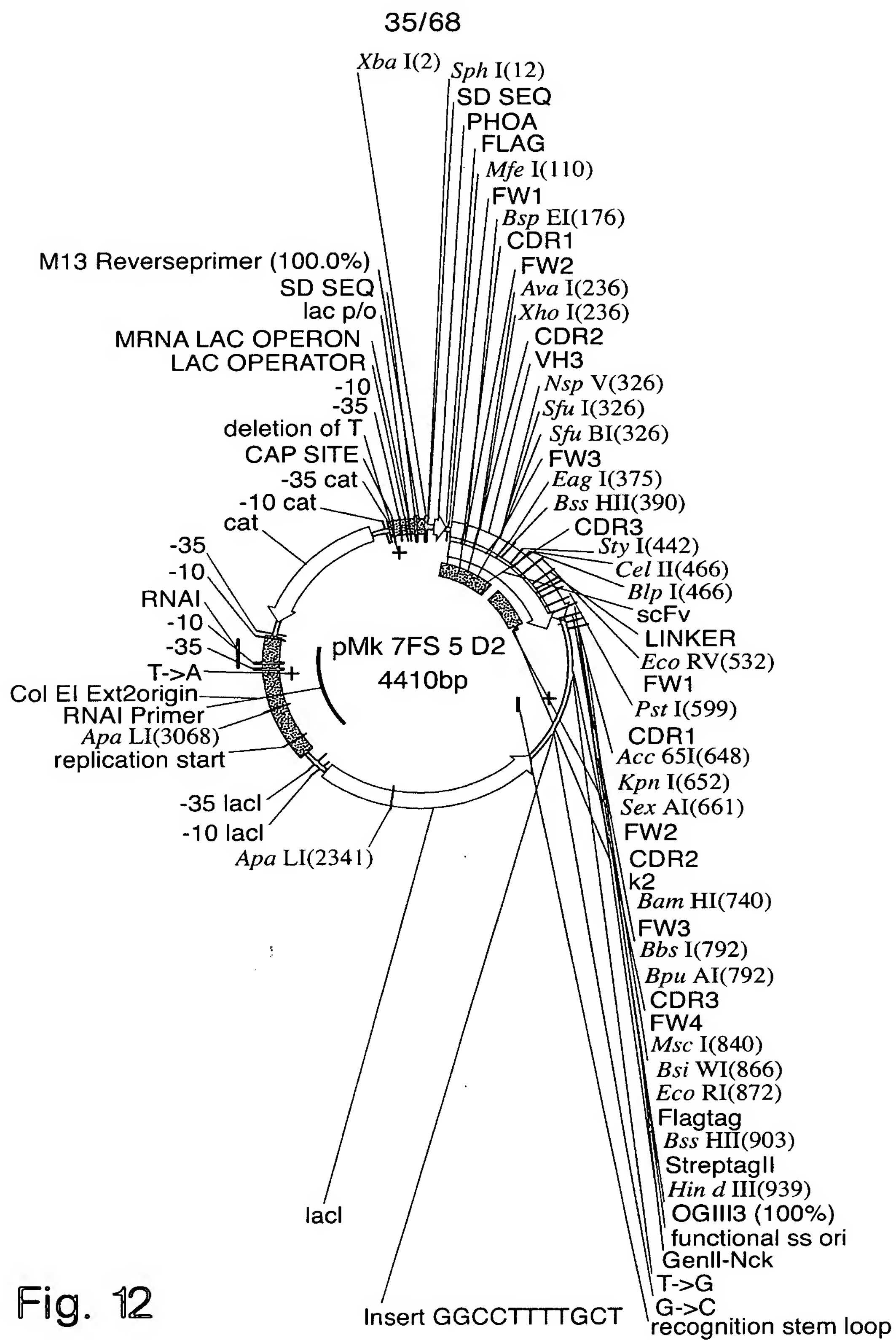


Fig. 12

```

      XbaI   SphI
      ~~~~~~
1    TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
    AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

51   GGCACCTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG
    CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

      MfeI
      ~~~~~~
101  ATGAAGTGCA ATTGGTGGAA AGCGGCGGCG GCCTGGTGCA ACCGGGCGGC
    TACTTCACGT TAACCACCTT TCGCCGCCGC CGGACCACGT TGGCCCGCCG

      BspEI
      ~~~~~~
151  AGCCTGCGTC TGAGCTGCGC GGCCTCCGGA TTTACCTTTA GCAGCTATGC
    TCGGACGCAG ACTCGACGCG CCGGAGGCCT AAATGGAAAT CGTCGATACG

      XhoI
      ~~~~~~
      AvaI
      ~~~~~~
201  GATGAGCTGG GTGCGCCAAG CCCCTGGGAA GGGTCTCGAG TGGGTGAGCG
    CTACTCGACC CACGCGGTTC GGGGACCCTT CCCAGAGCTC ACCCACTCGC

251  CGATTAGCGG TAGCGGCGGC AGCACCTATT ATGCGGATAG CGTGAAAGGC
    GCTAATCGCC ATCGCCGCCG TCGTGGATAA TACGCCTATC GCACTTTCCG

      BstBI
      ~~~~~~
      SfuI
      ~~~~~~
      NspV
      ~~~~~~
301  CGTTTTACCA TTTCACGTGA TAATTCGAAA AACACCCTGT ATCTGCAAAT
    GCAAATGGT AAAGTGCACT ATTAAGCTTT TTGTGGGACA TAGACGTTTA

      EagI           BssHII
      ~~~~~~       ~~~~~~
351  GAACAGCCTG CGTGCGGAAG ATACGGCCGT GTATTATTGC GCGCGTGTTA
    CTTGTCGGAC GCACGCCTTC TATGCCGGCA CATAATAACG CGCGCACAAT

      StyI
      ~~~~~~
401  AGAAGCATTT TTCTCGTAAG AATTGGTTTG ATTATTGGGG CCAAGGCACC
    TCTTCGTAAA AAGAGCATTC TTAACCAAAC TAATAACCCC GGTTC CGTG

```

Fig. 12 (cont.)

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                                B1pI
                                ~~~~~~
                                CelII
                                ~~~~~~
451  CTGGTGACGG  TTAGCTCAGC  GGGTGGCGGT  TCTGGCGGCG  GTGGGAGCGG
     GACCACTGCC  AATCGAGTCG  CCCACCGCCA  AGACCGCCGC  CACCCTCGCC

                                EcoRV
                                ~~~~~~
501  TGGCGGTGGT  TCTGGCGGTG  GTGGTTCCGA  TATCGTGATG  ACCCAGAGCC
     ACCGCCACCA  AGACCGCCAC  CACCAAGGCT  ATAGCACTAC  TGGGTCTCGG

                                PstI
                                ~~~~~~
551  CACTGAGCCT  GCCAGTGACT  CCGGGCGAGC  CTGCGAGCAT  TAGCTGCAGA
     GTGACTCGGA  CGGTCACTGA  GGCCCGCTCG  GACGCTCGTA  ATCGACGTCT

                                KpnI
                                ~~~~~~
                                Acc65I
                                ~~~~~~
601  AGCAGCCAAA  GCCTGCTGCA  TAGCAACGGC  TATAACTATC  TGGATTGGTA
     TCGTCGGTTT  CGGACGACGT  ATCGTTGCCG  ATATTGATAG  ACCTAACCAT

KpnI
~~
Acc65I      SexAI
~~          ~~~~~~
651  CCTTCAAAAA  CCAGGTCAAA  GCCCGCAGCT  ATTAATTTAT  CTGGGCAGCA
     GGAAGTTTTT  GGTCCAGTTT  CGGGCGTCGA  TAATTAAATA  GACCCGTCGT

                                BamHI
                                ~~~~~~
701  ACCGTGCCAG  TGGGGTCCCG  GATCGTTTTA  GCGGCTCTGG  ATCCGGCACC
     TGGCACGGTC  ACCCCAGGGC  CTAGCAAAAT  CGCCGAGACC  TAGGCCGTGG

                                BpuAI
                                ~~~~~~
                                BbsI
                                ~~~~~~
751  GATTTTACCC  TGAAAATTAG  CCGTGTGGAA  GCTGAAGACG  TGGGCGTGTA
     CTAAAATGGG  ACTTTTAATC  GGCACACCTT  CGACTTCTGC  ACCCGCACAT

                                MscI
                                ~~~~~~
801  TTATTGCCAG  CAGCATTATA  CCACCCCGCC  GACCTTTGGC  CAGGGTACGA
     AATAACGGTC  GTCGTAATAT  GGTGGGGCGG  CTGGAAACCG  GTCCCATGCT

```

Fig. 12-3

|      |            |                |             |             |            |
|------|------------|----------------|-------------|-------------|------------|
|      |            | BsiWI    EcoRI |             |             |            |
|      |            | ~~~~~          |             |             |            |
| 851  | AAGTTGAAAT | TAAACGTACG     | GAATTCGACT  | ATAAAGATGA  | CGATGACAAA |
|      | TTCAACTTTA | ATTTGCATGC     | CTTAAGCTGA  | TATTTCTACT  | GCTACTGTTT |
|      | BssHII     |                |             | HindIII     |            |
|      | ~~~~~      |                |             | ~~~~~       |            |
| 901  | GGCGCGCCGT | GGAGCCACCC     | GCAGTTTGAA  | AAATGATAAG  | CTTGACCTGT |
|      | CCGCGCGGCA | CCTCGGTGGG     | CGTCAAACCTT | TTTACTATTC  | GAAGTGGACA |
|      |            |                |             | OGIII3      | 100.0%     |
|      |            |                |             | =====       |            |
| 951  | GAAGTGAAAA | ATGGCGCAGA     | TTGTGCGACA  | TTTTTTTTTGT | CTGCCGTTTA |
|      | CTTCACTTTT | TACCGCGTCT     | AACACGCTGT  | AAAAAAAACA  | GACGGCAAAT |
|      | OGIII3     | 100.0%         |             |             |            |
|      | =====      |                |             |             |            |
| 1001 | ATTAAAGGGG | GGGGGGGGCC     | GGCCTGGGGG  | GGGGTGTACA  | TGAAATTGTA |
|      | TAATTTCCCC | CCCCCCCCCG     | CCGGACCCCC  | CCCCACATGT  | ACTTTAACAT |
| 1051 | AACGTTAATA | TTTTGTATAA     | ATTCGCGTTA  | AATTTTTGTT  | AAATCAGCTC |
|      | TTGCAATTAT | AAAACAATTT     | TAAGCGCAAT  | TTAAAAACAA  | TTTAGTCGAG |
| 1101 | ATTTTTTAAC | CAATAGGCCG     | AAATCGGCAA  | AATCCCTTAT  | AAATCAAAAG |
|      | TAAAAAATTG | GTTATCCGGC     | TTTAGCCGTT  | TTAGGGAATA  | TTTAGTTTTT |
| 1151 | AATAGACCGA | GATAGGGTTG     | AGTGTGTGTC  | CAGTTTGGA   | CAAGAGTCCA |
|      | TTATCTGGCT | CTATCCCAAC     | TCACAACAAG  | GTCAAACCTT  | GTTCTCAGGT |
| 1201 | CTATTAAAGA | ACGTGGACTC     | CAACGTCAAA  | GGGCGAAAAA  | CCGTCTATCA |
|      | GATAATTTCT | TGCACCTGAG     | GTTGCAGTTT  | CCCGCTTTTT  | GGCAGATAGT |
| 1251 | GGGCGATGGC | CCACTACGAG     | AACCATCACC  | CTAATCAAGT  | TTTTTGGGGT |
|      | CCCGCTACCG | GGTGATGCTC     | TTGGTAGTGG  | GATTAGTTCA  | AAAAACCCCA |
| 1301 | CGAGGTGCCG | TAAAGCACTA     | AATCGGAACC  | CTAAAGGGAG  | CCCCCGATTT |
|      | GCTCCACGGC | ATTTCTGTGAT    | TTAGCCTTGG  | GATTTCCCTC  | GGGGGCTAAA |
| 1351 | AGAGCTTGAC | GGGGAAAGCC     | GGCGAACGTG  | GCGAGAAAGG  | AAGGGAAGAA |
|      | TCTCGAACTG | CCCCTTTCGG     | CCGCTTGCAC  | CGCTCTTTCC  | TTCCCTTCTT |
| 1401 | AGCGAAAGGA | GCGGGCGCTA     | GGGCGCTGGC  | AAGTGTAGCG  | GTCACGCTGC |
|      | TCGCTTTCCT | CGCCCGCGAT     | CCCGCGACCG  | TTCACATCGC  | CAGTGCGACG |
| 1451 | GCGTAACCAC | CACACCCGCC     | GCGCTTAATG  | CGCCGCTACA  | GGGCGCGTGC |
|      | CGCATTTGGT | GTGTGGGCGG     | CGCGAATTAC  | GCGGCGATGT  | CCCGCGCACG |

Fig. 12 (cont.)

|      |                          |                           |                          |                          |                          |
|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|
| 1501 | TAGACTAGTG<br>ATCTGATCAC | TTTAAACCGG<br>AAATTTGGCC  | ACCGGGGGGG<br>TGGCCCCCCC | GGCTTAAGTG<br>CCGAATTCAC | GGCTGCAAAA<br>CCGACGTTTT |
| 1551 | CAAAACGGCC<br>GTTTTGCCGG | TCCTGTCAGG<br>AGGACAGTCC  | AAGCCGCTTT<br>TTCGGCGAAA | TATCGGGTAG<br>ATAGCCCATC | CCTCACTGCC<br>GGAGTGACGG |
| 1601 | CGCTTTCCAG<br>GCGAAAGGTC | TCGGGAAACC<br>AGCCCTTTGG  | TGTCGTGCCA<br>ACAGCACGGT | GCTGCATCAG<br>CGACGTAGTC | TGAATCGGCC<br>ACTTAGCCGG |
| 1651 | AACGCGCGGG<br>TTGCGCGCCC | GAGAGGCGGT<br>CTCTCCGCCA  | TTGCGTATTG<br>AACGCATAAC | GGAGCCAGGG<br>CCTCGGTCCC | TGGTTTTTCT<br>ACCAAAAAGA |
| 1701 | TTTCACCAGT<br>AAAGTGGTCA | GAGACGGGCA<br>CTCTGCCCCG  | ACAGCTGATT<br>TGTCGACTAA | GCCCTTCACC<br>CGGGAAGTGG | GCCTGGCCCT<br>CGGACCGGGA |
| 1751 | GAGAGAGTTG<br>CTCTCTCAAC | CAGCAAGCGG<br>GTCGTTTCGCC | TCCACGCTGG<br>AGGTGCGACC | TTTGCCCCAG<br>AAACGGGGTC | CAGGCGAAAA<br>GTCCGCTTTT |
| 1801 | TCCTGTTTGA<br>AGGACAAACT | TGGTGGTCAG<br>ACCACCAGTC  | CGGCGGGATA<br>GCCGCCCTAT | TAACATGAGC<br>ATTGTACTCG | TGTCCTCGGT<br>ACAGGAGCCA |
| 1851 | ATCGTCGTAT<br>TAGCAGCATA | CCCACTACCG<br>GGGTGATGGC  | AGATGTCCGC<br>TCTACAGGCG | ACCAACGCGC<br>TGGTTGCGCG | AGCCCGGACT<br>TCGGGCCTGA |
| 1901 | CGGTAATGGC<br>GCCATTACCG | ACGCATTGCG<br>TGCGTAACGC  | CCCAGCGCCA<br>GGGTCGCGGT | TCTGATCGTT<br>AGACTAGCAA | GGCAACCAGC<br>CCGTTGGTCG |
| 1951 | ATCGCAGTGG<br>TAGCGTCACC | GAACGATGCC<br>CTTGCTACGG  | CTCATTCAGC<br>GAGTAAGTCG | ATTTGCATGG<br>TAAACGTACC | TTTGTTGAAA<br>AAACAACTTT |
| 2001 | ACCGGACATG<br>TGGCCTGTAC | GCACTCCAGT<br>CGTGAGGTCA  | CGCCTTCCCG<br>GCGGAAGGGC | TTCCGCTATC<br>AAGGCGATAG | GGCTGAATTT<br>CCGACTTAAA |
| 2051 | GATTGCGAGT<br>CTAACGCTCA | GAGATATTTA<br>CTCTATAAAT  | TGCCAGCCAG<br>ACGGTCGGTC | CCAGACGCAG<br>GGTCTGCGTC | ACGCGCCGAG<br>TGCGCGGCTC |
| 2101 | ACAGAACTTA<br>TGTCTTGAAT | ATGGGCCAGC<br>TACCCGGTCC  | TAACAGCGCG<br>ATTGTGCGCG | ATTTGCTGGT<br>TAAACGACCA | GGCCCAATGC<br>CCGGGTACG  |
| 2151 | GACCAGATGC<br>CTGGTCTACG | TCCACGCCCA<br>AGGTGCGGGT  | GTCGCGTACC<br>CAGCGCATGG | GTCCTCATGG<br>CAGGAGTACC | GAGAAAATAA<br>CTCTTTTATT |
| 2201 | TACTGTTGAT<br>ATGACAACTA | GGGTGTCTGG<br>CCCACAGACC  | TCAGAGACAT<br>AGTCTCTGTA | CAAGAAATAA<br>GTTCTTTATT | CGCCGGAACA<br>GCGGCCTTGT |
| 2251 | TTAGTGCAGG<br>AATCACGTCC | CAGCTTCCAC<br>GTCGAAGGTG  | AGCAATAGCA<br>TCGTTATCGT | TCCTGGTCAT<br>AGGACCAGTA | CCAGCGGATA<br>GGTCGCCTAT |

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Fig. 12 (cont.)



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|      |                           |                           |                           |                           |                           |
|------|---------------------------|---------------------------|---------------------------|---------------------------|---------------------------|
| 2301 | GTTAATAATC<br>CAATTATTAG  | AGCCCACTGA<br>TCGGGTGACT  | CACGTTGCGC<br>GTGCAACGCG  | GAGAAGATTG<br>CTCTTCTAAC  | TGCACCGCCG<br>ACGTGGCGGC  |
| 2351 | CTTTACAGGC<br>GAAATGTCCG  | TTCGACGCCG<br>AAGCTGCGGC  | CTTCGTTCTA<br>GAAGCAAGAT  | CCATCGACAC<br>GGTAGCTGTG  | GACCACGCTG<br>CTGGTGCGAC  |
| 2401 | GCACCCAGTT<br>CGTGGGTCAA  | GATCGGCGCG<br>CTAGCCGCGC  | AGATTTAATC<br>TCTAAATTAG  | GCCGCGACAA<br>CGGCGCTGTT  | TTTGCGACGG<br>AAACGCTGCC  |
| 2451 | CGCGTGCAGG<br>GCGCACGTCC  | GCCAGACTGG<br>CGGTCTGACC  | AGGTGGCAAC<br>TCCACCGTTG  | GCCAATCAGC<br>CGGTTAGTCG  | AACGACTGTT<br>TTGCTGACAA  |
| 2501 | TGCCCCGCCAG<br>ACGGGCGGTC | TTGTTGTGCC<br>AACAAACACGG | ACGCGGTTAG<br>TGCGCCAATC  | GAATGTAATT<br>CTTACATTAA  | CAGCTCCGCC<br>GTCGAGGCGG  |
| 2551 | ATCGCCGCTT<br>TAGCGGCGAA  | CCACTTTTTTC<br>GGTGAAAAAG | CCGCGTTTTTC<br>GGCGCAAAAG | GCAGAAACGT<br>CGTCTTTGCA  | GGCTGGCCTG<br>CCGACCGGAC  |
| 2601 | G TTCACCACG<br>CAAGTGGTGC | C GGGAAACGG<br>GCCCTTTGCC | T CTGATAAGA<br>AGACTATTCT | G ACACCGGCA<br>CTGTGGCCGT | T ACTCTGCGA<br>ATGAGACGCT |
| 2651 | C ATCGTATAA<br>GTAGCATATT | C GTTACTGGT<br>GCAATGACCA | T TCACATTCA<br>AAGTGTAAGT | C CACCCTGAA<br>GGTGGGACTT | T TGACTCTCT<br>AACTGAGAGA |
| 2701 | T CCGGGCGCT<br>AGGCCCGCGA | A TCATGCCAT<br>TAGTACGGTA | A CCGCGAAAG<br>TGGCGCTTTC | G TTTTTCGCG<br>CAAAACGCGG | A TTCGATGCT<br>TAAGCTACGA |
| 2751 | A GCCATGTGA<br>TCGGTACACT | G CAAAAGGCC<br>CGTTTTCCGG | A GCAAAAGGC<br>TCGTTTTCCG | C AGGAACCGT<br>GTCCTTGGCA | A AAAAAGGCC<br>TTTTTCCGGC |
| 2801 | C GTTGCTGGC<br>GCAACGACCG | G TTTTTCCAT<br>CAAAAAGGTA | A GGCTCCGCC<br>TCCGAGGCGG | C CCCTGACGA<br>GGGGACTGCT | G CATCACAAA<br>CGTAGTGTTT |
| 2851 | A ATCGACGCT<br>TTAGCTGCGA | C AAGTCAGAG<br>GTTCAGTCTC | G TGGCGAAAC<br>CACCGCTTTG | C CGACAGGAC<br>GGCTGTCCTG | T ATAAAGATA<br>ATATTTCTAT |
| 2901 | C CAGGCGTTT<br>GGTCCGCAAA | C CCCCTGGAA<br>GGGGGACCTT | G CTCCTCGT<br>CGAGGGAGCA  | G CGCTCTCCT<br>CGCGAGAGGA | G TTCCGACCC<br>CAAGGCTGGG |
| 2951 | T GCCGCTTAC<br>ACGGCGAATG | C GGATACCTG<br>GCCTATGGAC | T CCGCCTTTC<br>AGGCGGAAAG | T CCCTTCGGG<br>AGGGAAGCCC | A AGCGTGGCG<br>TTCGCACCGC |
| 3001 | C TTTCTCATA<br>GAAAGAGTAT | G CTCACGCTG<br>CGAGTGCGAC | T AGGTATCTC<br>ATCCATAGAG | A GTTCGGTGT<br>TCAAGCCACA | A AGGTCGTTG<br>TCCAGCAAGC |

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|      |                           |                           |                           |                           |                            |
|------|---------------------------|---------------------------|---------------------------|---------------------------|----------------------------|
| 3051 | CTCCAAGCTG<br>GAGGTTCGAC  | GGCTGTGTGC<br>CCGACACACG  | ACGAACCCCC<br>TGCTTGGGGG  | CGTTCAGCCC<br>GCAAGTCGGG  | GACCGCTGCG<br>CTGGCGACGC   |
| 3101 | C CTTATCCGG<br>GGAATAGGCC | T AACTATCGT<br>ATTGATAGCA | C TTGAGTCCA<br>GAACTCAGGT | A CCCGGTAAG<br>TGGGCCATTC | A ACACGACTTA<br>TGTGCTGAAT |

Fig. 12 (cont.)



|      |                          |                          |                           |                           |                           |
|------|--------------------------|--------------------------|---------------------------|---------------------------|---------------------------|
| 3151 | TCGCCACTGG<br>AGCGGTGACC | CAGCAGCCAC<br>GTCGTCGGTG | TGGTAACAGG<br>ACCATTGTC   | ATTAGCAGAG<br>TAATCGTCTC  | CGAGGTATGT<br>GCTCCATACA  |
| 3201 | AGGCGGTGCT<br>TCCGCCACGA | ACAGAGTTCT<br>TGTCTCAAGA | TGAAGTGGTG<br>ACTTCACCAC  | GCCTAACTAC<br>CGGATTGATG  | GGCTACACTA<br>CCGATGTGAT  |
| 3251 | GAAGAACAGT<br>CTTCTTGTC  | ATTTGGTATC<br>TAAACCATAG | TGCGCTCTGC<br>ACGCGAGACG  | TGTAGCCAGT<br>ACATCGGTCA  | TACCTTCGGA<br>ATGGAAGCCT  |
| 3301 | AAAAGAGTTG<br>TTTTCTCAAC | GTAGCTCTTG<br>CATCGAGAAC | ATCCGGCAAA<br>TAGGCCGTTT  | CAAACCACCG<br>GTTTGGTGGC  | CTGGTAGCGG<br>GACCATCGCC  |
| 3351 | TGGTTTTTTT<br>ACCAAAAAAA | GTTTGCAAGC<br>CAAACGTTTC | AGCAGATTAC<br>TCGTCTAATG  | GCGCAGAAAA<br>CGCGTCTTTT  | AAAGGATCTC<br>TTTCCTAGAG  |
| 3401 | AAGAAGATCC<br>TTCTTCTAGG | TTTGATCTTT<br>AAACTAGAAA | TCTACGGGGT<br>AGATGCCCCA  | CTGACGCTCA<br>GACTGCGAGT  | GTGGAACGAA<br>CACCTTGCTT  |
| 3451 | AACTCACGTT<br>TTGAGTGCAA | AAGGGATTTT<br>TTCCCTAAAA | GGTCAGATCT<br>CCAGTCTAGA  | AGCACCAGGC<br>TCGTGGTCCG  | GTTTAAGGGC<br>CAAATTCCCG  |
| 3501 | ACCAATAACT<br>TGGTTATTGA | GCCTTAAAAA<br>CGGAATTTTT | AATTACGCCC<br>TTAATGCGGG  | CGCCCTGCCA<br>GCGGGACGGT  | CTCATCGCAG<br>GAGTAGCGTC  |
| 3551 | TACTGTTGTA<br>ATGACAACAT | ATTCATTAAG<br>TAAGTAATTC | CATTCTGCCG<br>GTAAGACGGC  | ACATGGAAGC<br>TGTACCTTCG  | CATCACAAAC<br>GTAGTGTTTG  |
| 3601 | GGCATGATGA<br>CCGTACTACT | ACCTGAATCG<br>TGGACTTAGC | CCAGCGGCAT<br>GGTCGCCGTA  | CAGCACCTTG<br>GTCGTGGAAC  | TCGCCTTGCG<br>AGCGGAACGC  |
| 3651 | TATAATATTT<br>ATATTATAAA | GCCCATAGTG<br>CGGGTATCAC | AAAACGGGGG<br>TTTTGCCCCC  | CGAAGAAGTT<br>GCTTCTTCAA  | GTCCATATTG<br>CAGGTATAAC  |
| 3701 | GCTACGTTTA<br>CGATGCAAAT | AATCAAAACT<br>TTAGTTTTGA | GGTGAAACTC<br>CCTTTTGAG   | ACCCAGGGAT<br>TGGGTCCCTA  | TGGCTGAGAC<br>ACCGACTCTG  |
| 3751 | GAAAAACATA<br>CTTTTTGTAT | TTCTCAATAA<br>AAGAGTTATT | ACCCTTTAGG<br>TGGGAAATCC  | GAAATAGGCC<br>CTTTATCCGG  | AGGTTTTTCAC<br>TCCAAAAGTG |
| 3801 | CGTAACACGC<br>GCATTGTGCG | CACATCTTGC<br>GTGTAGAACG | GAATATATGT<br>CTTATATACA  | GTAGAAACTG<br>CATCTTTGAC  | CCGGAAATCG<br>GGCCTTTAGC  |
| 3851 | TCGTGGTATT<br>AGCACCATAA | CACTCCAGAG<br>GTGAGGTCTC | CGATGAAAAC<br>GCTACTTTTG  | GTTTCAGTTT<br>CAAAGTCAAA  | GTCATGGAA<br>CGAGTACCTT   |
| 3901 | AACGGTGTA<br>TTGCCACATT  | CAAGGGTGAA<br>GTTCCCACTT | CACTATCCCA<br>GTGATAGGGT  | TATCACCAGC<br>ATAGTGGTCTG | TCACCGTCTT<br>AGTGGCAGAA  |
| 3951 | TCATTGCCAT<br>AGTAACGGTA | ACGGAACTCC<br>TGCCTTGAGG | GGGTGAGCAT<br>CCCACCTCGTA | TCATCAGGCG<br>AGTAGTCCGC  | GGCAAGAATG<br>CCGTTCTTAC  |

Fig. 12 (cont.)

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4001  TGAATAAAGG  CCGGATAAAA  CTTGTGCTTA  TTTTCTTTA  CGGTCTTTAA
      ACTTATTTCC  GGCCTATTTT  GAACACGAAT  AAAAAGAAAT  GCCAGAAATT

4051  AAAGGCCGTA  ATATCCAGCT  GAACGGTCTG  GTTATAGGTA  CATTGAGCAA
      TTTCCGGCAT  TATAGGTCGA  CTTGCCAGAC  CAATATCCAT  GTAACTCGTT

4101  CTGACTGAAA  TGCCTCAAAA  TGTTCCTTAC  GATGCCATTG  GGATATATCA
      GACTGACTTT  ACGGAGTTTT  ACAAGAAATG  CTACGGTAAC  CCTATATAGT

4151  ACGGTGGTAT  ATCCAGTGAT  TTTTTTCTCC  ATTTTAGCTT  CCTTAGCTCC
      TGCCACCATA  TAGGTCACTA  AAAAAGAGG  TAAAATCGAA  GGAATCGAGG

4201  TGAAAATCTC  GATAACTCAA  AAAATACGCC  CGGTAGTGAT  CTTATTTTCAT
      ACTTTTAGAG  CTATTGAGTT  TTTTATGCGG  GCCATCACTA  GAATAAAGTA

4251  TATGGTGAAA  GTTGGAACCT  CACCCGACGT  CTAATGTGAG  TTAGCTCACT
      ATACCACTTT  CAACCTTGGA  GTGGGCTGCA  GATTACACTC  AATCGAGTGA

4301  CATTAGGCAC  CCCAGGCTTT  ACACTTTATG  CTTCCGGCTC  GTATGTTGTG
      GTAATCCGTG  GGGTCCGAAA  TGTGAAATAC  GAAGGCCGAG  CATAACAACAC

                                     M13 Reverse primer 100.0%
                                     =====
4351  TGGAATTGTG  AGCGGATAAC  AATTTACACAC  AGGAAACAGC  TATGACCATG
      ACCTTAACAC  TCGCCTATTG  TTAAAGTGTG  TCCTTTGTCTG  ATACTGGTAC

4401  ATTACGAATT
      TAATGCTTAA

```

Fig. 12 (cont.)

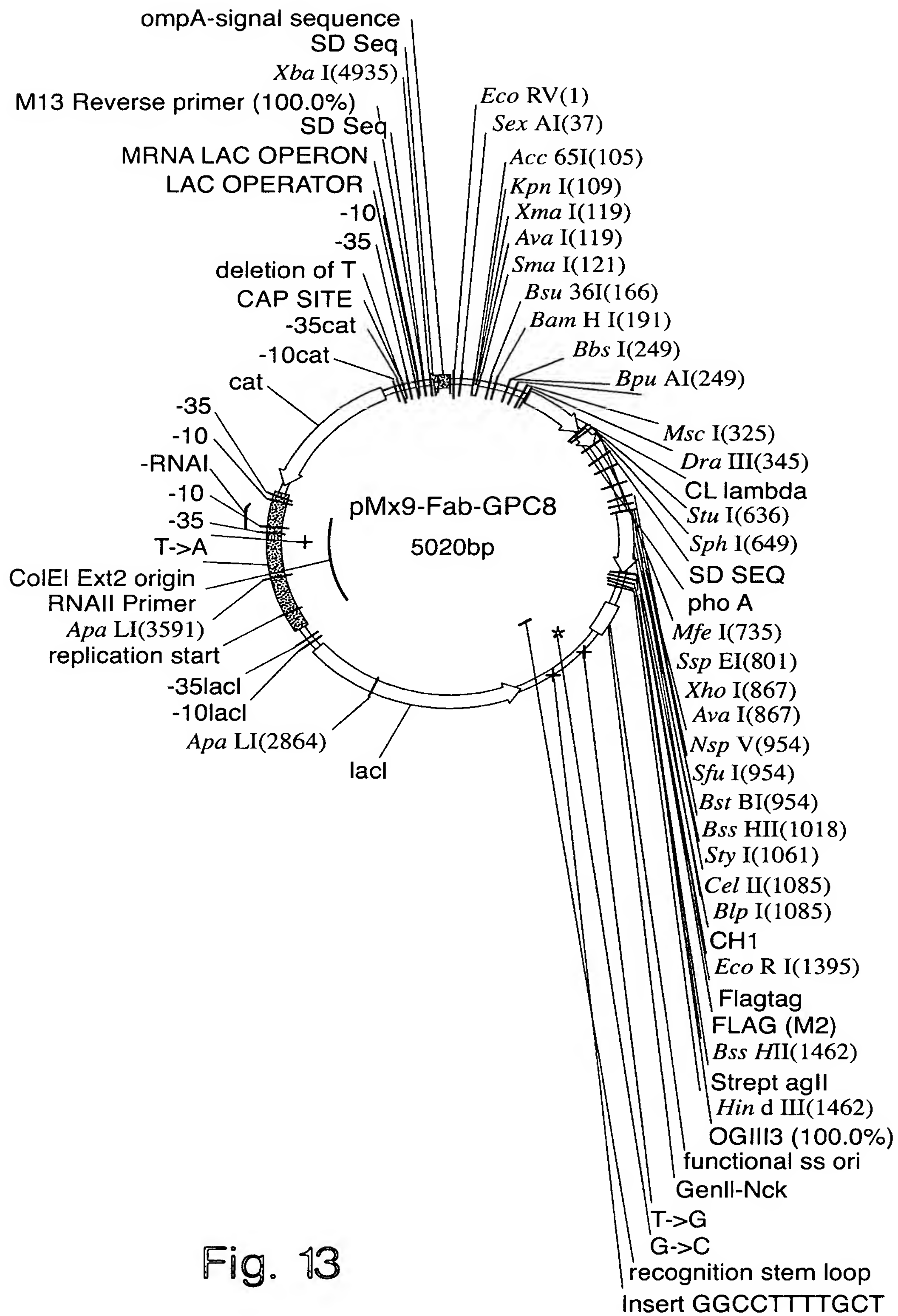


Fig. 13

|     |            |             |            |            |            |
|-----|------------|-------------|------------|------------|------------|
|     | EcoRV      |             |            |            | SexAI      |
|     | ~~~~       |             |            |            | ~~~~~      |
| 1   | ATCGTGCTGA | CCCAGCCGCC  | TTCAGTGAGT | GGCGCACCAG | GTCAGCGTGT |
|     | TAGCACGACT | GGGTCGGCGG  | AAGTCACTCA | CCGCGTGGTC | CAGTCGCACA |
| 51  | GACCATCTCG | TGTAGCGGCA  | GCAGCAGCAA | CATTGGCAGC | AACTATGTGA |
|     | CTGGTAGAGC | ACATCGCCGT  | CGTCGTCGTT | GTAACCGTCG | TTGATACT   |
|     |            | XmaI        |            |            |            |
|     |            | ~~~~~       |            |            |            |
|     | KpnI       | SmaI        |            |            |            |
|     | ~~~~~      | ~~~~~       |            |            |            |
|     | Acc65I     | AvaI        |            |            |            |
|     | ~~~~~      | ~~~~~       |            |            |            |
| 101 | GCTGGTACCA | GCAGTTGCC   | GGGACGGCGC | CGAAACTGCT | GATTTATGAT |
|     | CGACCATGGT | CGTCAACGGG  | CCCTGCCGCG | GCTTTGACGA | CTAAATACTA |
|     |            | Bsu36I      |            |            | BamHI      |
|     |            | ~~~~~       |            |            | ~~~~~      |
| 151 | AACAACCAGC | GTCCCTCAGG  | CGTGCCGGAT | CGTTTTAGCG | GATCCAAAAG |
|     | TTGTTGGTCG | CAGGGAGTCC  | GCACGGCCTA | GCAAATCGC  | CTAGGTTTTT |
|     |            |             |            | BpuAI      |            |
|     |            |             |            | ~~~~~      |            |
|     |            |             |            | BbsI       |            |
|     |            |             |            | ~~~~~      |            |
| 201 | CGGCACCAGC | GCGAGCCTTG  | CGATTACGGG | CCTGCAAAGC | GAAGACGAAG |
|     | GCCGTGGTCG | CGCTCGGAAC  | GCTAATGCCC | GGACGTTTCG | CTTCTGCTTC |
|     |            |             | Bsu36I     |            |            |
|     |            |             | ~~~~~      |            |            |
| 251 | CGGATTATTA | TTGCCAGAGC  | TATGACATGC | CTCAGGCTGT | GTTTGGCGGC |
|     | GCCTAATAAT | AACGGTCTCG  | ATACTGTACG | GAGTCCGACA | CAAACCGCCG |
|     |            | MscI        |            |            | DraIII     |
|     |            | ~~~~~       |            |            | ~~~~~      |
| 301 | GGCACGAAGT | TTAACCGTTC  | TTGGCCAGCC | GAAAGCCGCA | CCGAGTGTGA |
|     | CCGTGCTTCA | AATTGGCAAG  | AACCGGTCGG | CTTTCGGCGT | GGCTCACACT |
| 351 | CGCTGTTTCC | GCCGAGCAGC  | GAAGAATTGC | AGGCGAACAA | AGCGACCCTG |
|     | GCGACAAAGG | CGGCTCGTCG  | CTTCTTAACG | TCCGCTTGTT | TCGCTGGGAC |
| 401 | GTGTGCCTGA | TTAGCGACTT  | TTATCCGGGA | GCCGTGACAG | TGGCCTGGAA |
|     | CACACGGACT | AATCGCTGAA  | AATAGGCCCT | CGGCACTGTC | ACCGGACCTT |
| 451 | GGCAGATAGC | AGCCCCGTCA  | AGGCGGGAGT | GGAGACCACC | ACACCCTCCA |
|     | CCGTCTATCG | TCGGGGCAGT  | TCCGCCCTCA | CCTCTGGTGG | TGTGGGAGGT |
| 501 | AACAAAGCAA | CAACAAGTAC  | GCGGCCAGCA | GCTATCTGAG | CCTGACGCCT |
|     | TTGTTTCGTT | GTTGTTTCATG | CGCCGGTCGT | CGATAGACTC | GGACTGCGGA |

Fig. 13 (cont.)

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|      |            |            |            |            |            |
|------|------------|------------|------------|------------|------------|
| 551  | GAGCAGTGGA | AGTCCCACAG | AAGCTACAGC | TGCCAGGTCA | CGCATGAGGG |
|      | CTCGTCACCT | TCAGGGTGTC | TTCGATGTCG | ACGGTCCAGT | GCGTACTCCC |
|      |            |            | StuI       | SphI       |            |
|      |            |            | ~~~~~      | ~~~~~      |            |
| 601  | GAGCACCGTG | GAAAAAACCG | TTGCGCCGAC | TGAGGCCTGA | TAAGCATGCG |
|      | CTCGTGGCAC | CTTTTTTGGC | AACGCGGCTG | ACTCCGGACT | ATTCGTACGC |
| 651  | TAGGAGAAAA | TAAAATGAAA | CAAAGCACTA | TTGCACTGGC | ACTCTTACCG |
|      | ATCCTCTTTT | ATTTTACTTT | GTTTCGTGAT | AACGTGACCG | TGAGAATGGC |
|      |            |            | MfeI       |            |            |
|      |            |            | ~~~~~      |            |            |
| 701  | TTGCTCTTCA | CCCCTGTTAC | CAAAGCCCAG | GTGCAATTGA | AAGAAAGCGG |
|      | AACGAGAAGT | GGGGACAATG | GTTTCGGGTC | CACGTTAACT | TTCTTTCGCC |
|      |            |            |            | BspEI      |            |
|      |            |            |            | ~          |            |
| 751  | CCCGGCCCTG | GTGAAACCGA | CCCAAACCCT | GACCCTGACC | TGTACCTTTT |
|      | GGGCCGGGAC | CACTTTGGCT | GGGTTTGGGA | CTGGGACTGG | ACATGGAAAA |
|      | BspEI      |            |            |            |            |
|      | ~~~~~      |            |            |            |            |
| 801  | CCGGATTTAG | CCTGTCCACG | TCTGGCGTTG | GCGTGGGCTG | GATTCGCCAG |
|      | GGCCTAAATC | GGACAGGTGC | AGACCGCAAC | CGCACCCGAC | CTAAGCGGTC |
|      |            | XhoI       |            |            |            |
|      |            | ~~~~~      |            |            |            |
|      |            | AvaI       |            |            |            |
|      |            | ~~~~~      |            |            |            |
| 851  | CCGCCTGGGA | AAGCCCTCGA | GTGGCTGGCT | CTGATTGATT | GGGATGATGA |
|      | GGCGGACCCT | TTCGGGAGCT | CACCGACCGA | GACTAACTAA | CCCTACTACT |
| 901  | TAAGTATTAT | AGCACCAGCC | TGAAAACGCG | TCTGACCATT | AGCAAAGATA |
|      | ATTCATAATA | TCGTGGTCGG | ACTTTTGCGC | AGACTGGTAA | TCGTTTCTAT |
|      | BstBI      |            |            |            |            |
|      | ~~~~~      |            |            |            |            |
|      | SfuI       |            |            |            |            |
|      | ~~~~~      |            |            |            |            |
|      | NspV       |            |            |            |            |
|      | ~~~~~      |            |            |            |            |
| 951  | CTTCGAAAAA | TCAGGTGGTG | CTGACTATGA | CCAACATGGA | CCCGGTGGAT |
|      | GAAGCTTTTT | AGTCCACCAC | GACTGATACT | GGTTGTACCT | GGGCCACCTA |
|      |            | BssHII     |            |            |            |
|      |            | ~~~~~      |            |            |            |
| 1001 | ACGGCCACCT | ATTATTGCGC | GCGTTCTCCT | CGTTATCGTG | GTGCTTTTGA |
|      | TGCCGGTGGA | TAATAACGCG | CGCAAGAGGA | GCAATAGCAC | CACGAAAAC  |
|      |            |            | BlpI       |            |            |

Fig. 13 (cont.)

|      |            |            |            |             |             |
|------|------------|------------|------------|-------------|-------------|
|      |            | StyI       |            |             | ~~~~~       |
|      |            | ~~~~~      |            |             | CelII       |
|      |            | ~~~~~      |            |             | ~~~~~       |
| 1051 | TTATTGGGGC | CAAGGCACCC | TGGTGACGGT | TAGCTCAGCG  | TCGACCAAAG  |
|      | AATAACCCCG | GTTCCGTGGG | ACCACTGCCA | ATCGAGTCGC  | AGCTGGTTTC  |
| 1101 | GTCCAAGCGT | GTTTCCGCTG | GCTCCGAGCA | GCAAAAGCAC  | CAGCGGCGGC  |
|      | CAGGTTTCGA | CAAAGGCGAC | CGAGGCTCGT | CGTTTTTCGTG | GTCGCCGCCG  |
| 1151 | ACGGCTGCCC | TGGGCTGCCT | GGTTAAAGAT | TATTTCCCGG  | AACCAGTCAC  |
|      | TGCCGACGGG | ACCCGACGGA | CCAATTTCTA | ATAAAGGGCC  | TTGGTCAGTG  |
| 1201 | CGTGAGCTGG | AACAGCGGGG | CGCTGACCAG | CGGCGTG CAT | ACCTTTCCGG  |
|      | GCACTCGACC | TTGTCGCCCC | GCGACTGGTC | GCCGCACGTA  | TGGAAAGGCC  |
| 1251 | CGGTGCTGCA | AAGCAGCGGC | CTGTATAGCC | TGAGCAGCGT  | TGTGACCGTG  |
|      | GCCACGACGT | TTCGTCGCCG | GACATATCGG | ACTCGTCGCA  | ACACTGGCAC  |
| 1301 | CCGAGCAGCA | GCTTAGGCAC | TCAGACCTAT | ATTTGCAACG  | TGAACCATAA  |
|      | GGCTCGTCGT | CGAATCCGTG | AGTCTGGATA | TAAACGTTGC  | ACTTGGTATT  |
|      |            |            |            |             | EcoRI       |
|      |            |            |            |             | ~~~~~       |
| 1351 | ACCGAGCAAC | ACCAAAGTGG | ATAAAAAAGT | GGAACCGAAA  | AGCGAATTCG  |
|      | TGGCTCGTTG | TGGTTTCACC | TATTTTTTCA | CCTTGGCTTT  | TCGCTTAAGC  |
|      |            |            | BssHII     |             |             |
|      |            |            | ~~~~~      |             |             |
| 1401 | ACTATAAAGA | TGACGATGAC | AAAGGCGCGC | CGTGGAGCCA  | CCCGCAGTTT  |
|      | TGATATTTCT | ACTGCTACTG | TTTCCGCGCG | GCACCTCGGT  | GGGCGTCAAA  |
|      |            | HindIII    |            |             |             |
|      |            | ~~~~~      |            |             |             |
| 1451 | GAAAAATGAT | AAGCTTGACC | TGTGAAGTGA | AAAATGGCGC  | AGATTGTGCG  |
|      | CTTTTTACTA | TTCGAACTGG | ACACTTCACT | TTTTACCGCG  | TCTAACACGC  |
|      |            | OGIII3     | 100.0%     |             |             |
|      |            | =====      |            |             |             |
| 1501 | ACATTTTTTT | TGTCTGCCGT | TTAATTAAAG | GGGGGGGGGG  | GCCGGCCTGG  |
|      | TGTAAAAAAA | ACAGACGGCA | AATTAATTTT | CCCCCCCCCC  | CGGCCGGACC  |
| 1551 | GGGGGGGTGT | ACATGAAATT | GTAAACGTTA | ATATTTTGTT  | AAAATTCGCG  |
|      | CCCCCCCACA | TGTACTTTAA | CATTTGCAAT | TATAAAACAA  | TTTTAAGCGC  |
| 1601 | TTAAATTTTT | GTAAATCAG  | CTCATTTTTT | AACCAATAGG  | CCGAAATCGG  |
|      | AATTTAAAAA | CAATTTAGTC | GAGTAAAAAA | TTGGTTATCC  | GGCTTTAGCC  |
| 1651 | CAAAATCCCT | TATAAATCAA | AAGAATAGAC | CGAGATAGGG  | TTGAGTGTTG  |
|      | GTTTTAGGGA | ATATTTAGTT | TTCTTATCTG | GCTCTATCCC  | AACTCACAAAC |
| 1701 | TTCCAGTTTG | GAACAAGAGT | CCACTATTAA | AGAACGTGGA  | CTCCAACGTC  |
|      | AAGGTCAAAC | CTTGTTCTCA | GGTGATAATT | TCTTGACACT  | GAGGTGTCAG  |

Fig. 13 (cont.)



|      |                          |                          |                          |                           |                          |
|------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|
| 1751 | AAAGGGCGAA<br>TTTCCCGCTT | AAACCGTCTA<br>TTTGGCAGAT | TCAGGGCGAT<br>AGTCCCGCTA | GGCCCACTAC<br>CCGGGTGATG  | GAGAACCATC<br>CTCTTGGTAG |
| 1801 | ACCCTAATCA<br>TGGGATTAGT | AGTTTTTTTG<br>TCAAAAACC  | GGTCGAGGTG<br>CCAGCTCCAC | CCGTAAAGCA<br>GGCATTTTCGT | CTAAATCGGA<br>GATTTAGCCT |
| 1851 | ACCCTAAAGG<br>TGGGATTTCC | GAGCCCCCGA<br>CTCGGGGGCT | TTTAGAGCTT<br>AAATCTCGAA | GACGGGGAAA<br>CTGCCCTTT   | GCCGGCGAAC<br>CGGCCGCTTG |
| 1901 | GTGGCGAGAA<br>CACCGCTCTT | AGGAAGGGAA<br>TCCTTCCCTT | GAAAGCGAAA<br>CTTTCGCTTT | GGAGCGGGCG<br>CCTCGCCCGC  | CTAGGGCGCT<br>GATCCCGCGA |
| 1951 | GGCAAGTGTA<br>CCGTTCACAT | GCGGTCACGC<br>CGCCAGTGCG | TGCGCGTAAC<br>ACGCGCATTG | CACCACACCC<br>GTGGTGTGGG  | GCCGCGCTTA<br>CGGCGCGAAT |
| 2001 | ATGCGCCGCT<br>TACGCGGCGA | ACAGGGCGCG<br>TGTCCCGCGC | TGCTAGACTA<br>ACGATCTGAT | GTGTTTAAAC<br>CACAAATTTG  | CGGACCGGGG<br>GCCTGGCCCC |
| 2051 | GGGGGCTTAA<br>CCCCGAATT  | GTGGGCTGCA<br>CACCCGACGT | AAACAAAACG<br>TTTGTTTTGC | GCCTCCTGTC<br>CGGAGGACAG  | AGGAAGCCGC<br>TCCTTCGGCG |
| 2101 | TTTTATCGGG<br>AAAATAGCCC | TAGCCTCACT<br>ATCGGAGTGA | GCCCGCTTTC<br>CGGGCGAAAG | CAGTCGGGAA<br>GTCAGCCCTT  | ACCTGTCGTG<br>TGGACAGCAC |
| 2151 | CCAGCTGCAT<br>GGTCGACGTA | CAGTGAATCG<br>GTCACCTAGC | GCCAACGCGC<br>CGGTTGCGCG | GGGGAGAGGC<br>CCCCTCTCCG  | GGTTTGCGTA<br>CCAAACGCAT |
| 2201 | TTGGGAGCCA<br>AACCCTCGGT | GGGTGGTTTT<br>CCCACCAAAA | TCTTTTCACC<br>AGAAAAGTGG | AGTGAGACGG<br>TCACTCTGCC  | GCAACAGCTG<br>CGTTGTGAC  |
| 2251 | ATTGCCCTTC<br>TAACGGGAAG | ACCGCCTGGC<br>TGGCGGACCG | CCTGAGAGAG<br>GGACTCTCTC | TTGCAGCAAG<br>AACGTCGTTC  | CGGTCCACGC<br>GCCAGGTGCG |
| 2301 | TGGTTTGCCC<br>ACCAAACGGG | CAGCAGGCGA<br>GTCGTCCGCT | AAATCCTGTT<br>T'TAGGACAA | TGATGGTGGT<br>ACTACCACCA  | CAGCGGCGGG<br>GTCGCCGCC  |
| 2351 | ATATAACATG<br>TATATTGTAC | AGCTGTCCTC<br>TCGACAGGAG | GGTATCGTCG<br>CCATAGCAGC | TATCCCACTA<br>ATAGGGTGAT  | CCGAGATGTC<br>GGCTCTACAG |
| 2401 | CGCACCAACG<br>GCGTGGTTGC | CGCAGCCCGG<br>GCGTCGGGCC | ACTCGGTAAT<br>TGAGCCATTA | GGCACGCATT<br>CCGTGCGTAA  | GCGCCACGCG<br>CGCGGGTCGC |
| 2451 | CCATCTGATC<br>GGTAGACTAG | GTTGGCAACC<br>CAACCGTTGG | AGCATCGCAG<br>TCGTAGCGTC | TGGGAACGAT<br>ACCCTTGCTA  | GCCCTCATTC<br>CGGGAGTAAG |
| 2501 | AGCATTTGCA<br>TCGTAAACGT | TGGTTTGTTG<br>ACCAAACAAC | AAAACCGGAC<br>TTTTGGCCTG | ATGGCACTCC<br>TACCGTGAGG  | AGTCGCCTTC<br>TCAGCGGAAG |
| 2551 | CCGTTCCGCT<br>GGCAAGGCGA | ATCGGCTGAA<br>TAGCCGACTT | TTTGATTGCG<br>AAACTAACGC | AGTGAGATAT<br>TCACTCTATA  | TTATGCCAGC<br>AATACGGTCG |

Fig. 13 (cont.)

|      |                          |                          |                          |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 2601 | CAGCCAGACG<br>GTCGGTCTGC | CAGACGCGCC<br>GTCTGCGCGG | GAGACAGAAC<br>CTCTGTCTTG | TTAATGGGCC<br>AATTACCCGG | AGCTAACAGC<br>TCGATTGTCG |
| 2651 | GCGATTTGCT<br>CGCTAAACGA | GGTGGCCCAA<br>CCACCGGGTT | TGCGACCAGA<br>ACGCTGGTCT | TGCTCCACGC<br>ACGAGGTGCG | CCAGTCGCGT<br>GGTCAGCGCA |
| 2701 | ACCGTCCTCA<br>TGGCAGGAGT | TGGGAGAAAA<br>ACCCTCTTTT | TAATACTGTT<br>ATTATGACAA | GATGGGTGTC<br>CTACCCACAG | TGGTCAGAGA<br>ACCAGTCTCT |
| 2751 | CATCAAGAAA<br>GTAGTTCTTT | TAACGCCGGA<br>ATTGCGGCCT | ACATTAGTGC<br>TGTAATCACG | AGGCAGCTTC<br>TCCGTCGAAG | CACAGCAATA<br>GTGTCGTTAT |
| 2801 | GCATCCTGGT<br>CGTAGGACCA | CATCCAGCGG<br>GTAGGTCGCC | ATAGTTAATA<br>TATCAATTAT | ATCAGCCCAC<br>TAGTCGGGTG | TGACACGTTG<br>ACTGTGCAAC |
|      |                          | ApaLI<br>~~~~~           |                          |                          |                          |
| 2851 | CGCGAGAAGA<br>GCGCTCTTCT | TTGTGCACCG<br>AACACGTGGC | CCGCTTTACA<br>GGCGAAATGT | GGCTTCGACG<br>CCGAAGCTGC | CCGCTTCGTT<br>GGCGAAGCAA |
| 2901 | CTACCATCGA<br>GATGGTAGCT | CACGACCACG<br>GTGCTGGTGC | CTGGCACCCA<br>GACCGTGGGT | GTTGATCGGC<br>CAACTAGCCG | GCGAGATTTA<br>CGCTCTAAAT |
| 2951 | ATCGCCGCGA<br>TAGCGGCGCT | CAATTTGCGA<br>GTAAACGCT  | CGGCGCGTGC<br>GCCGCGCACG | AGGGCCAGAC<br>TCCCGGTCTG | TGGAGGTGGC<br>ACCTCCACCG |
| 3001 | AACGCCAATC<br>TTGCGGTTAG | AGCAACGACT<br>TCGTTGCTGA | GTTTGCCCGC<br>CAAACGGGCG | CAGTTGTTGT<br>GTCAACAACA | GCCACGCGGT<br>CGGTGCGCCA |
| 3051 | TAGGAATGTA<br>ATCCTTACAT | ATTCAGCTCC<br>TAAGTCGAGG | GCCATCGCCG<br>CGGTAGCGGC | CTTCCACTTT<br>GAAGGTGAAA | TTCCCGCGTT<br>AAGGGCGCAA |
| 3101 | TTCGCAGAAA<br>AAGCGTCTTT | CGTGGCTGGC<br>GCACCGACCG | CTGGTTCACC<br>GACCAAGTGG | ACGCGGGAAA<br>TGCGCCCTTT | CGGTCTGATA<br>GCCAGACTAT |
| 3151 | AGAGACACCG<br>TCTCTGTGGC | GCATACTCTG<br>CGTATGAGAC | CGACATCGTA<br>GCTGTAGCAT | TAACGTTACT<br>ATTGCAATGA | GGTTTCACAT<br>CCAAAGTGTA |
| 3201 | TCACCACCCT<br>AGTGGTGGGA | GAATTGACTC<br>CTTAACTGAG | TCTTCCGGGC<br>AGAAGGCCCG | GCTATCATGC<br>CGATAGTACG | CATACCGCGA<br>GTATGGCGCT |
| 3251 | AAGGTTTTGC<br>TTCCAAAACG | GCCATTCGAT<br>CGGTAAGCTA | GCTAGCCATG<br>CGATCGGTAC | TGAGCAAAAG<br>ACTCGTTTTT | GCCAGCAAAA<br>CGGTCGTTTT |
| 3301 | GGCCAGGAAC<br>CCGGTCCTTG | CGTAAAAAGG<br>GCATTTTTTC | CCGCGTTGCT<br>GGCGCAACGA | GGCGTTTTTC<br>CCGCAAAAAG | CATAGGCTCC<br>GTATCCGAGG |
| 3351 | GCCCCCTGA<br>CGGGGGGACT  | CGAGCATCAC<br>GCTCGTAGTG | AAAAATCGAC<br>TTTTTAGCTG | GCTCAAGTCA<br>CGAGTTCAGT | GAGGTGGCGA<br>CTCCACCGCT |
| 3401 | AACCCGACAG               | GACTATAAAG               | ATACCAGGCG               | TTTCCCCCTG               | GAAGCTCCCT               |

Fig. 13 (cont.)



|      |                          |                          |                          |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
|      | TTGGGCTGTC               | CTGATATTTT               | TATGGTCCGC               | AAAGGGGGAC               | CTTCGAGGGA               |
| 3451 | CGTGCGCTCT<br>GCACGCGAGA | CCTGTTCCGA<br>GGACAAGGCT | CCCTGCCGCT<br>GGGACGGCGA | TACCGGATAC<br>ATGGCCTATG | CTGTCCGCCT<br>GACAGGCGGA |
| 3501 | TTCTCCCTTC<br>AAGAGGGAAG | GGGAAGCGTG<br>CCCTTCGCAC | GCGCTTTCTC<br>CGCGAAAGAG | ATAGCTCACG<br>TATCGAGTGC | CTGTAGGTAT<br>GACATCCATA |
|      |                          |                          |                          | ApaLI<br>~~~~~           |                          |
| 3551 | CTCAGTTCGG<br>GAGTCAAGCC | TGTAGGTCGT<br>ACATCCAGCA | TCGCTCCAAG<br>AGCGAGGTTC | CTGGGCTGTG<br>GACCCGACAC | TGCACGAACC<br>ACGTGCTTGG |
| 3601 | CCCCGTTTCA<br>GGGGCAAGTC | CCCGACCGCT<br>GGGCTGGCGA | GCGCCTTATC<br>CGCGGAATAG | CGGTAACAT<br>GCCATTGATA  | CGTCTTGAGT<br>GCAGAACTCA |
| 3651 | CCAACCCGGT<br>GGTTGGGCCA | AAGACACGAC<br>TTCTGTGCTG | TTATCGCCAC<br>AATAGCGGTG | TGGCAGCAGC<br>ACCGTCGTCG | CACTGGTAAC<br>GTGACCATTG |
| 3701 | AGGATTAGCA<br>TCCTAATCGT | GAGCGAGGTA<br>CTCGCTCCAT | TGTAGGCGGT<br>ACATCCGCCA | GCTACAGAGT<br>CGATGTCTCA | TCTTGAAGTG<br>AGAACTTCAC |
| 3751 | GTGGCCTAAC<br>CACCGGATTG | TACGGCTACA<br>ATGCCGATGT | CTAGAAGAAC<br>GATCTTCTTG | AGTATTTGGT<br>TCATAAACCA | ATCTGCGCTC<br>TAGACGCGAG |
| 3801 | TGCTGTAGCC<br>ACGACATCGG | AGTTACCTTC<br>TCAATGGAAG | GGAAAAAGAG<br>CCTTTTTCTC | TTGGTAGCTC<br>AACCATCGAG | TTGATCCGGC<br>AACTAGGCCG |
| 3851 | AAACAAACCA<br>TTTGTTTGGT | CCGCTGGTAG<br>GGCGACCATC | CGGTGGTTTT<br>GCCACCAAAA | TTTGTTTGCA<br>AAACAAACGT | AGCAGCAGAT<br>TCGTCGTCTA |
| 3901 | TACGCGCAGA<br>ATGCGCGTCT | AAAAAAGGAT<br>TTTTTTCCTA | CTCAAGAAGA<br>GAGTTCTTCT | TCCTTTGATC<br>AGGAAACTAG | TTTTCTACGG<br>AAAAGATGCC |
| 3951 | GGTCTGACGC<br>CCAGACTGCG | TCAGTGGAAC<br>AGTCACCTTG | GAAAACTCAC<br>CTTTTGAGTG | GTTAAGGGAT<br>CAATTCCCTA | TTTGGTCAGA<br>AAACCAGTCT |
| 4001 | TCTAGCACCA<br>AGATCGTGGT | GGCGTTTAAG<br>CCGCAAATTC | GGCACCAATA<br>CCGTGGTTAT | ACTGCCTTAA<br>TGACGGAATT | AAAAATTACG<br>TTTTTAATGC |
| 4051 | CCCCGCCCTG<br>GGGGCGGGAC | CCACTCATCG<br>GGTGAGTAGC | CAGTACTGTT<br>GTCATGACAA | GTAATTCATT<br>CATTAAGTAA | AAGCATTCTG<br>TTCGTAAGAC |
| 4101 | CCGACATGGA<br>GGCTGTACCT | AGCCATCACA<br>TCGGTAGTGT | AACGGCATGA<br>TTGCCGTACT | TGAACCTGAA<br>ACTTGGAATT | TCGCCAGCGG<br>AGCGGTCGCC |
| 4151 | CATCAGCACC<br>GTAGTCGTGG | TTGTGCGCTT<br>AACAGCGGAA | GCGTATAATA<br>CGCATATTAT | TTTGCCCAT<br>AAACGGGTAT  | GTGAAAACGG<br>CACTTTTGCC |
| 4201 | GGGCGAAGAA<br>CCCGCTTCTT | GTTGTCCATA<br>CAACAGGTAT | TTGGCTACGT<br>AACCGATGCA | TTAAATCAAA<br>AATTTAGTTT | ACTGGTGAAA<br>TGACCACTTT |

Fig. 13 (cont.)

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|      |                           |             |            |            |            |
|------|---------------------------|-------------|------------|------------|------------|
| 4251 | CTCACCCAGG                | GATTGGCTGA  | GACGAAAAAC | ATATTCTCAA | TAAACCCTTT |
|      | GAGTGGGTCC                | CTAACCGACT  | CTGCTTTTTG | TATAAGAGTT | ATTTGGGAAA |
| 4301 | AGGGAAATAG                | GCCAGGTTTT  | CACCGTAACA | CGCCACATCT | TGCGAATATA |
|      | TCCCTTTATC                | CGGTCCAAAA  | GTGGCATTGT | GCGGTGTAGA | ACGCTTATAT |
| 4351 | TGTGTAGAAA                | CTGCCGGAAA  | TCGTCGTGGT | ATTCACTCCA | GAGCGATGAA |
|      | ACACATCTTT                | GACGGCCTTT  | AGCAGCACCA | TAAGTGAGGT | CTCGCTACTT |
| 4401 | AACGTTTCAG                | TTTGCTCATG  | GAAAACGGTG | TAACAAGGGT | GAACACTATC |
|      | TTGCAAAGTC                | AAACGAGTAC  | CTTTTGCCAC | ATTGTTCCCA | CTTGTGATAG |
| 4451 | CCATATCACC                | AGCTCACCGT  | CTTTCATTGC | CATACGGAAC | TCCGGGTGAG |
|      | GGTATAGTGG                | TCGAGTGGCA  | GAAAGTAACG | GTATGCCTTG | AGGCCCACTC |
| 4501 | CATTCATCAG                | GCGGGCAAGA  | ATGTGAATAA | AGGCCGGATA | AAACTTGTGC |
|      | GTAAGTAGTC                | CGCCCGTTCT  | TACACTTATT | TCCGGCCTAT | TTTGAACACG |
| 4551 | TTATTTTTCT                | TTACGGTCTT  | TAAAAAGGCC | GTAATATCCA | GCTGAACGGT |
|      | AATAAAAAGA                | AATGCCAGAA  | ATTTTTCGGG | CATTATAGGT | CGACTTGCCA |
| 4601 | CTGGTTATAG                | GTACATTGAG  | CAACTGACTG | AAATGCCTCA | AAATGTTCTT |
|      | GACCAATATC                | CATGTAACCTC | GTTGACTGAC | TTTACGGAGT | TTTACAAGAA |
| 4651 | TACGATGCCA                | TTGGGATATA  | TCAACGGTGG | TATATCCAGT | GATTTTTTTC |
|      | ATGCTACGGT                | AACCCCTATAT | AGTTGCCACC | ATATAGGTCA | CTAAAAAAG  |
| 4701 | TCCATTTTAG                | CTTCCTTAGC  | TCCTGAAAAT | CTCGATAACT | CAAAAAATAC |
|      | AGGTAAAATC                | GAAGGAATCG  | AGGACTTTTA | GAGCTATTGA | GTTTTTTATG |
| 4751 | GCCCGGTAGT                | GATCTTATTT  | CATTATGGTG | AAAGTTGGAA | CCTCACCCGA |
|      | CGGGCCATCA                | CTAGAATAAA  | GTAATACCAC | TTTCAACCTT | GGAGTGGGCT |
| 4801 | CGTCTAATGT                | GAGTTAGCTC  | ACTCATTAGG | CACCCCAGGC | TTTACACTTT |
|      | GCAGATTACA                | CTCAATCGAG  | TGAGTAATCC | GTGGGGTCCG | AAATGTGAAA |
| 4851 | ATGCTTCCGG                | CTCGTATGTT  | GTGTGGAATT | GTGAGCGGAT | AACAATTTCA |
|      | TACGAAGGCC                | GAGCATACAA  | CACACCTTAA | CACTCGCCTA | TTGTTAAAGT |
|      | M13 Reverse primer 100.0% |             |            | XbaI       |            |
|      | =====                     |             |            | ~~~~~      |            |
| 4901 | CACAGGAAAC                | AGCTATGACC  | ATGATTACGA | ATTTCTAGAT | AACGAGGGCA |
|      | GTGTCCTTTG                | TCGATACTGG  | TACTAATGCT | TAAAGATCTA | TTGCTCCCGT |
| 4951 | AAAAATGAAA                | AAGACAGCTA  | TCGCGATTGC | AGTGGCACTG | GCTGGTTTCG |
|      | TTTTTACTTT                | TTCTGTCGAT  | AGCGCTAACG | TCACCGTGAC | CGACCAAAGC |
|      | EcoRV                     |             |            |            |            |
|      | ~~~                       |             |            |            |            |
| 5001 | CTACCGTAGC                | GCAGGCCGAT  |            |            |            |
|      | GATGGCATCG                | CGTCCGGCTA  |            |            |            |

Fig. 13 (cont.)

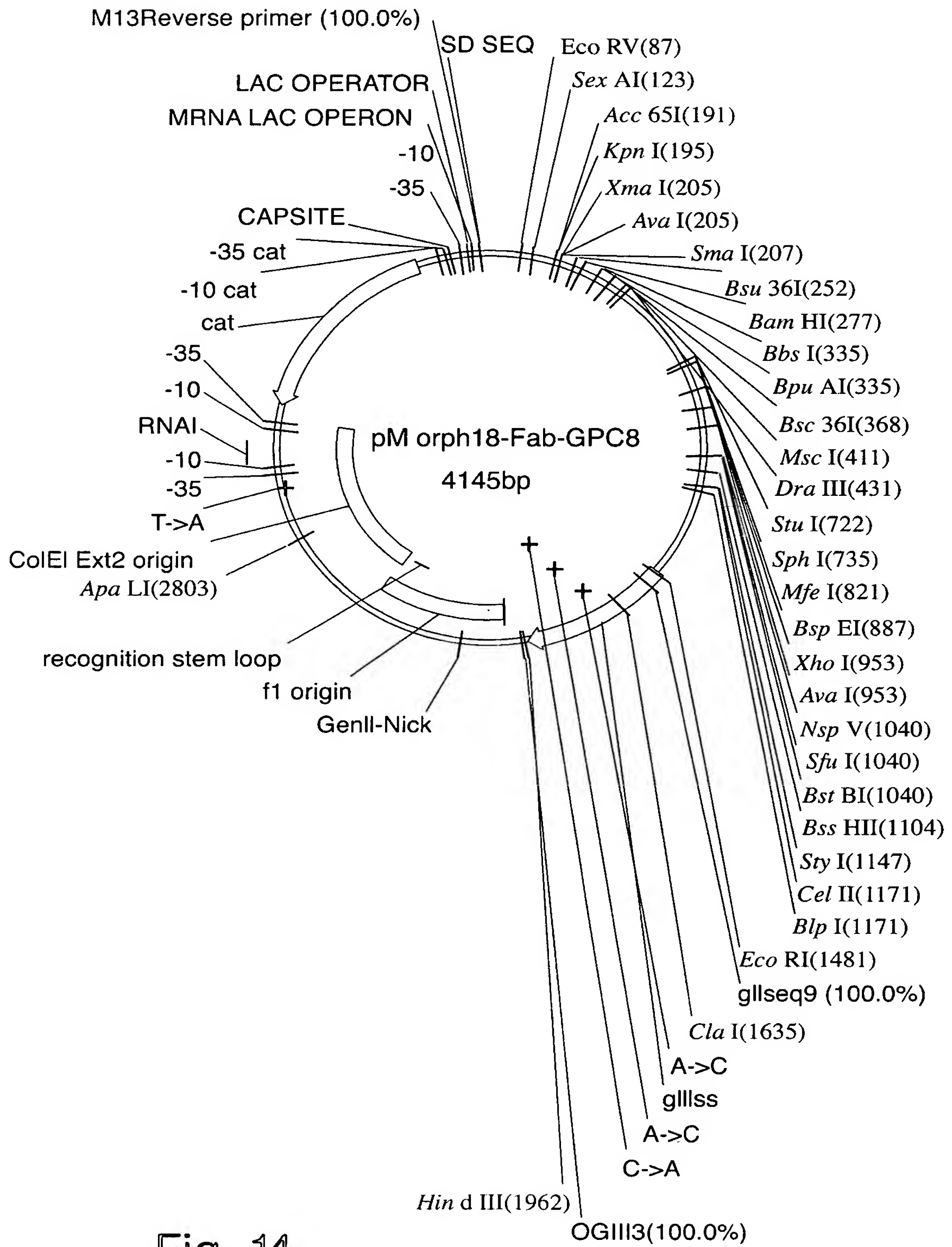


Fig. 14

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1  TCAGATAACG AGGGCAAAAA ATGAAAAAGA CAGCTATCGC GATTGCAGTG
   AGTCTATTGC TCCCGTTTTT TACTTTTTTCT GTCGATAGCG CTAACGTCAC

                                     EcoRV
                                     ~~~~~~
51  GCACTGGCTG GTTTCGCTAC CGTAGCGCAG GCCGATATCG TGCTGACCCA
   CGTGACCGAC CAAAGCGATG GCATCGCGTC CGGCTATAGC ACGACTGGGT

                                     SexAI
                                     ~~~~~~
101 GCCGCCTTCA GTGAGTGGCG CACCAGGTCA GCGTGTGACC ATCTCGTGTA
   CGGCGGAAGT CACTCACCGC GTGGTCCAGT CGCACACTGG TAGAGCACAT

                                     KpnI
                                     ~~~~~~
                                     Acc65I
                                     ~~~~~~
151 GCGGCAGCAG CAGCAACATT GGCAGCAACT ATGTGAGCTG GTACCAGCAG
   CGCCGTCGTC GTCGTTGTAA CCGTCGTTGA TACACTCGAC CATGGTCGTC

      XmaI
      ~~~~~~
      SmaI
      ~~~~~~
      AvaI
      ~~~~~~
                                     Bsu36I
                                     ~~~~~~
201 TTGCCC GGGA CGGCGCCGAA ACTGCTGATT TATGATAACA ACCAGCGTCC
   AACGGGCCCT GCCGCGGCTT TGACGACTAA ATACTATTGT TGGTCGCAGG

      Bsu36I
      ~~~~~~
                                     BamHI
                                     ~~~~~~
251 CTCAGGCGTG CCGGATCGTT TTAGCGGATC CAAAAGCGGC ACCAGCGCGA
   GAGTCCGCAC GGCCTAGCAA AATCGCCTAG GTTTTCGCCG TGGTCGCGCT

                                     BpuAI
                                     ~~~~~~
                                     BbsI
                                     ~~~~~~
301 GCCTTGCGAT TACGGGCCTG CAAAGCGAAG ACGAAGCGGA TTATTATTGC
   CGGAACGCTA ATGCCCGGAC GTTTCGCTTC TGCTTCGCCT AATAATAACG

                                     Bsu36I
                                     ~~~~~~
351 CAGAGCTATG ACATGCCTCA GGCTGTGTTT GGCGGCGGCA CGAAGTTTAA
   GTCTCGATAC TGTACGGAGT CCGACACAAA CCGCCGCCGT GCTTCAAATT

      MscI
      ~~~~~~
                                     DraIII
                                     ~~~~~~
401 CCGTTCTTGG CCAGCCGAAA GCCGCACCGA GTGTGACGCT GTTTCGCCG
   GGCAAGAACC GGTCGGCTTT CGGCGTGGCT CACACTGCGA CAAAGGCGGC

451 AGCAGCGAAG AATTGCAGGC GAACAAAGCG ACCCTGGTGT GCCTGATTAG
   TCGTCGCTTC TTAACGTCCG CTTGTTTCGC TGGGACCACA CGGACTAATC

501 CGACTTTTAT CCGGGAGCCG TGACAGTGGC CTGGAAGGCA GATAGCAGCC

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Fig. 14 (cont.)

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|      |            |            |            |            |            |
|------|------------|------------|------------|------------|------------|
|      | GCTGAAAATA | GGCCCTCGGC | ACTGTCACCG | GACCTTCCGT | CTATCGTCGG |
| 551  | CCGTCAAGGC | GGGAGTGGAG | ACCACCACAC | CCTCCAAACA | AAGCAACAAC |
|      | GGCAGTTCCG | CCCTCACCTC | TGGTGGTGTG | GGAGGTTTGT | TTCGTTGTTG |
| 601  | AAGTACGCGG | CCAGCAGCTA | TCTGAGCCTG | ACGCCTGAGC | AGTGGAAGTC |
|      | TTCATGCGCC | GGTCGTCGAT | AGACTCGGAC | TGCGGACTCG | TCACCTTCAG |
| 651  | CCACAGAAGC | TACAGCTGCC | AGGTCACGCA | TGAGGGGAGC | ACCGTGGAAG |
|      | GGTGTCTTCG | ATGTCGACGG | TCCAGTGCGT | ACTCCCCTCG | TGGCACCTTT |
|      |            | StuI       |            | SphI       |            |
|      |            | ~~~~~      |            | ~~~~~      |            |
| 701  | AAACCGTTGC | GCCGACTGAG | GCCTGATAAG | CATGCGTAGG | AGAAAATAAA |
|      | TTTGGCAACG | CGGCTGACTC | CGGACTATTC | GTACGCATCC | TCTTTTATTT |
| 751  | ATGAAACAAA | GCACTATTGC | ACTGGCACTC | TTACCGTTGC | TCTTCACCCC |
|      | TACTTTGTTT | CGTGATAACG | TGACCGTGAG | AATGGCAACG | AGAAGTGGGG |
|      |            | MfeI       |            |            |            |
|      |            | ~~~~~      |            |            |            |
| 801  | TGTTACCAAA | GCCCAGGTGC | AATTGAAAGA | AAGCGGCCCG | GCCCTGGTGA |
|      | ACAATGGTTT | CGGGTCCACG | TTAACTTTCT | TTCGCCGGGC | CGGGACCACT |
|      |            |            |            | BspEI      |            |
|      |            |            |            | ~~~~~      |            |
| 851  | AACCGACCCA | AACCCTGACC | CTGACCTGTA | CCTTTTCCGG | ATTTAGCCTG |
|      | TTGGCTGGGT | TTGGGACTGG | GACTGGACAT | GGAAAAGGCC | TAAATCGGAC |
| 901  | TCCACGTCTG | GCGTTGGCGT | GGGCTGGATT | CGCCAGCCGC | CTGGGAAAGC |
|      | AGGTGCAGAC | CGCAACCGCA | CCCGACCTAA | GCGGTCGGCG | GACCCTTTCG |
|      |            | XhoI       |            |            |            |
|      |            | ~~~~~      |            |            |            |
|      |            | AvaI       |            |            |            |
|      |            | ~~~~~      |            |            |            |
| 951  | CCTCGAGTGG | CTGGCTCTGA | TTGATTGGGA | TGATGATAAG | TATTATAGCA |
|      | GGAGCTCACC | GACCGAGACT | AACTAACCCT | ACTACTATTC | ATAATATCGT |
|      |            |            |            | BstBI      |            |
|      |            |            |            | ~~~~~      |            |
|      |            |            |            | SfuI       |            |
|      |            |            |            | ~~~~~      |            |
|      |            |            |            | NspV       |            |
|      |            |            |            | ~~~~~      |            |
| 1001 | CCAGCCTGAA | AACGCGTCTG | ACCATTAGCA | AAGATACTTC | GAAAAATCAG |
|      | GGTCGGACTT | TTGCGCAGAC | TGGTAATCGT | TTCTATGAAG | CTTTTATAGT |
| 1051 | GTGGTGCTGA | CTATGACCAA | CATGGACCCG | GTGGATACGG | CCACCTATTA |
|      | CACCACGACT | GATACTGGTT | GTACCTGGGC | CACCTATGCC | GGTGGATAAT |
|      |            | BssHII     |            |            | StyI       |
|      |            | ~~~~~      |            |            | ~~~~~      |
| 1101 | TTGCGCGCGT | TCTCCTCGTT | ATCGTGGTGC | TTTTGATTAT | TGGGGCCAAG |
|      | AACGCGCGCA | AGAGGAGCAA | TAGCACCACG | AAAATAATA  | ACCCCGGTTC |

B1pI

Fig. 14 (cont.)

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StyI

CelII

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|      |                          |                          |                          |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 1151 | GCACCCTGGT<br>CGTGGGACCA | GACGGTTAGC<br>CTGCCAATCG | TCAGCGTCGA<br>AGTCGCAGCT | CCAAAGGTCC<br>GGTTTCCAGG | AAGCGTGTTT<br>TTCGCACAAA |
| 1201 | CCGCTGGCTC<br>GGCGACCGAG | CGAGCAGCAA<br>GCTCGTCGTT | AAGCACCAGC<br>TTCGTGGTCG | GGCGGCACGG<br>CCGCCGTGCC | CTGCCCTGGG<br>GACGGGACCC |
| 1251 | CTGCCTGGTT<br>GACGGACCAA | AAAGATTATT<br>TTTCTAATAA | TCCCGGAACC<br>AGGGCCTTGG | AGTCACCGTG<br>TCAGTGGCAC | AGCTGGAACA<br>TCGACCTTGT |
| 1301 | GCGGGGCGCT<br>CGCCCCGCGA | GACCAGCGGC<br>CTGGTCGCCG | GTGCATACCT<br>CACGTATGGA | TTCCGGCGGT<br>AAGGCCGCCA | GCTGCAAAGC<br>CGACGTTTCG |
| 1351 | AGCGGCCTGT<br>TCGCCGGACA | ATAGCCTGAG<br>TATCGGACTC | CAGCGTTGTG<br>GTCGCAACAC | ACCGTGCCGA<br>TGGCACGGCT | GCAGCAGCTT<br>CGTCGTGCGA |
| 1401 | AGGCACTCAG<br>TCCGTGAGTC | ACCTATATTT<br>TGGATATAAA | GCAACGTGAA<br>CGTTGCACTT | CCATAAACCG<br>GGTATTTGGC | AGCAACACCA<br>TCGTTGTGGT |

EcoRI

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|      |                          |                          |                          |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 1451 | AAGTGGATAA<br>TTCACCTATT | AAAAGTGGAA<br>TTTTACCTT  | CCGAAAAGCG<br>GGCTTTTCGC | AATTCGGGGG<br>TTAAGCCCCC | AGGGAGCGGG<br>TCCCTCGCCC |
| 1501 | AGCGGTGATT<br>TCGCCACTAA | TTGATTATGA<br>AACTAATACT | AAAGATGGCA<br>TTTCTACCGT | AACGCTAATA<br>TTGCGATTAT | AGGGGGCTAT<br>TCCCCGATA  |

gIIIseq9 100.0%

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|      |                          |                          |                          |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 1551 | GACCGAAAAT<br>CTGGCTTTTA | GCCGATGAAA<br>CGGCTACTTT | ACGCGCTACA<br>TGCGCGATGT | GTCTGACGCT<br>CAGACTGCGA | AAAGGCAAAC<br>TTTCCGTTTG |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|

ClaI

~~~~~

|      |                          |                          |                          |                          |                           |
|------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|
| 1601 | TTGATTCTGT<br>AACTAAGACA | CGCTACTGAT<br>GCGATGACTA | TACGGTGCTG<br>ATGCCACGAC | CTATCGATGG<br>GATAGCTACC | TTTCATTGGT<br>AAAGTAACCA  |
| 1651 | GACGTTTCCG<br>CTGCAAAGGC | GCCTTGCTAA<br>CGGAACGATT | TGGTAATGGT<br>ACCATTACCA | GCTACTGGTG<br>CGATGACCAC | ATTTTGCTGG<br>TAAACGACC   |
| 1701 | CTCTAATTCC<br>GAGATTAAGG | CAAATGGCTC<br>GTTTACCGAG | AAGTCGGTGA<br>TTCAGCCACT | CGGTGATAAT<br>GCCACTATTA | TCACCTTTAA<br>AGTGGAATT   |
| 1751 | TGAATAATTT<br>ACTTATTAAA | CCGTCAATAT<br>GGCAGTTATA | TTACCTTCCC<br>AATGGAAGGG | TCCCTCAATC<br>AGGGAGTTAG | GGTTGAATGT<br>CCAACCTTACA |
| 1801 | CGCCCTTTTG<br>GCGGGAAAAC | TCTTTGGCGC<br>AGAAACCGCG | TGGTAAACCA<br>ACCATTGTTG | TATGAATTTT<br>ATACTTAAAA | CTATTGATTG<br>GATAACTAAC  |
| 1851 | TGACAAAATA<br>ACTGTTTTAT | AACTTATTCC<br>TTGAATAAGG | GTGGTGTCTT<br>CACCACAGAA | TGCGTTTCTT<br>ACGCAAAGAA | TTATATGTTG<br>AATATACAAC  |
| 1901 | CCACCTTTAT<br>GGTGGAAATA | GTATGTATTT<br>CATACATAAA | TCTACGTTTG<br>AGATGCAAAC | CTAACATACT<br>GATTGTATGA | GCGTAATAAG<br>CGCATTATTC  |

Fig. 14 (cont.)



## HindIII

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1951  GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
      CTCAGAACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
              OGIII3 100.0%
              =====

2001  ACATTTTTTTT TGTCTGCCGT TTAATGAAAT TGTAACGTT AATATTTTGT
      TGTAACAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

2051  TAAAATTTCGC GTTAAATTTT TGTAAATCA GCTCATTTTT TAACCAATAG
      ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

2101  GCCGAAATCG GCAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
      CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

2151  GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
      CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC

2201  ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
      TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

2251  CGAGAACCAT CACCCTAATC AAGTTTTTTTG GGGTCGAGGT GCCGTAAAGC
      GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG

2301  ACTAAATCGG AACCCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
      TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCTT

2351  AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC
      TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCG

2401  GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC
      CGATCCCGCG ACCGTTTACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

2451  CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA
      GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT ACACTCGTTT

2501  AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTTT
      TCCGGTCGTT TTCCGGTCCT TGGCATTTTTT CCGGCGCAAC GACCGCAAAA

2551  TCCATAGGCT CCGCCCCCCT GACGAGCATC AAAAAAATCG ACGCTCAAGT
      AGGTATCCGA GCGGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA

2601  CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC
      GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2651  TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT
      ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2701  ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA
      TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2751  CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG
      GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC

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## ApaLI

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Fig. 14 (cont.)

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|            |                           |                          |                           |                           |                          |
|------------|---------------------------|--------------------------|---------------------------|---------------------------|--------------------------|
| 2801       | TGTGCACGAA<br>ACACGTGCTT  | CCCCCGTTC<br>GGGGGGCAAG  | AGTCCGACCG<br>TCAGGCTGGC  | CTGCGCCTTA<br>GACGCGGAAT  | TCCGGTAACT<br>AGGCCATTGA |
| 2851       | ATCGTCTTGA<br>TAGCAGAACT  | GTCCAACCCG<br>CAGGTTGGGC | GTAAGACACG<br>CATCTGTGTC  | ACTTATCGCC<br>TGAATAGCGG  | ACTGGCAGCA<br>TGACCGTCGT |
| 2901       | GCCACTGGTA<br>CGGTGACCAT  | ACAGGATTAG<br>TGTCCTAATC | CAGAGCGAGG<br>GTCTCGCTCC  | TATGTAGGCG<br>ATACATCCGC  | GTGCTACAGA<br>CACGATGTCT |
| 2951       | GTTCTTGAAG<br>CAAGAACTTC  | TGGTGGCCTA<br>ACCACCGGAT | ACTACGGCTA<br>TGATGCCGAT  | CACTAGAAGA<br>GTGATCTTCT  | ACAGTATTTG<br>TGTCAATAAC |
| 3001       | GSTATCTGCGC<br>CATAGACGCG | TCTGCTGTAG<br>AGACGACATC | CCAGTTACCT<br>GGTCAATGGA  | TCGGAAAAAG<br>AGCCTTTTTTC | AGTTGGTAGC<br>TCAACCATCG |
| 3051       | TCTTGATCCG<br>AGAACTAGGC  | GCAAACAAAC<br>CGTTTGTTTG | CACCGCTGGT<br>GTGGCGACCA  | AGCGGTGGTT<br>TCGCCACCAA  | TTTTTGTTTG<br>AAAAACAAAC |
| 3101       | CAAGCAGCAG<br>GTTGTCGTC   | ATTACGCGCA<br>TAATGCGCGT | GAAAAAAAGG<br>CTTTTTTTTCC | ATCTCAAGAA<br>TAGAGTTCTT  | GATCCTTTGA<br>CTAGGAAACT |
| 3151       | TCTTTTCTAC<br>AGAAAAGATG  | GGGGTCTGAC<br>CCCCAGACTG | GCTCAGTGGA<br>CGAGTCACCT  | ACGAAAACCTC<br>TGCTTTTGAG | ACGTTAAGGG<br>TGCAATTCCC |
| 3201       | ATTTTGGTCA<br>TAAAACCAGT  | GATCTAGCAC<br>CTAGATCGTG | CAGGCGTTTA<br>GTCCGCAAAT  | AGGGCACCAA<br>TCCCGTGGTT  | TAACTGCCTT<br>ATTGACGGAA |
| 3251       | AAAAAAATTA<br>TTTTTTTAAT  | CGCCCCGCC<br>GCGGGGCGGG  | TGCCACTCAT<br>ACGGTGAGTA  | CGCAGTACTG<br>GCGTCATGAC  | TTGTAATTCA<br>AACATTAAGT |
| 3301       | TTAAGCATTC<br>AATTCGTAAG  | TGCCGACATG<br>ACGGCTGTAC | GAAGCCATCA<br>CTTCGGTAGT  | CAAACGGCAT<br>GTTTGCCGTA  | GATGAACCTG<br>CTACTTGGAC |
| 3351       | AATCGCCAGC<br>TTAGCGGTCG  | GGCATCAGCA<br>CCGTAGTCGT | CCTTGTCGCC<br>GGAACAGCGG  | TTGCGTATAA<br>AACGCATATT  | TATTTGCCCA<br>ATAAACGGGT |
| 3401       | TAGTGAAAAC<br>ATCACTTTTG  | GGGGGCGAAG<br>CCCCCGCTTC | AAGTTGTCCA<br>TTCAACAGGT  | TATTGGCTAC<br>ATAACCGATG  | GTTTAAATCA<br>CAAATTTAGT |
| 3451       | AAACTGGTGA<br>TTTGACCACT  | AACTCACCCA<br>TTGAGTGGGT | GGGATTGGCT<br>CCCTAACCGA  | GAGACGAAAA<br>CTCTGCTTTT  | ACATATTCTC<br>TGTATAAGAG |
| 3501       | AATAAACCCCT<br>TTATTTGGGA | TTAGGGAAAT<br>AATCCCTTTA | AGGCCAGGTT<br>TCCGGTCCAA  | TTCACCGTAA<br>AAGTGGCATT  | CACGCCACAT<br>GTGCGGTGTA |
| 3551       | CTTGCGAATA<br>GAACGCTTAT  | TATGTGTAGA<br>ATACACATCT | AACTGCCGGA<br>TTGACGGCCT  | AATCGTCGTG<br>TTAGCAGCAC  | GTATTCACTC<br>CATAAGTGAG |
| +1<br>3601 | CAGAGCGATG<br>GTCTCGCTAC  | AAAACGTTTC<br>TTTTGCAAAG | AGTTTGCTCA<br>TCAAACGAGT  | TGGAAAACGG<br>ACCTTTTGCC  | TGTAACAAGG<br>ACATTGTTCC |
| 3651       | GTGAACACTA<br>CACTTGTGAT  | TCCCATATCA<br>AGGGTATAGT | CCAGCTCACC<br>GGTCGAGTGG  | GTCTTTCATT<br>CAGAAAGTAA  | GCCATACGGA<br>CGGTATGCCT |

Fig. 14 (cont.)



|      |                           |             |             |            |            |
|------|---------------------------|-------------|-------------|------------|------------|
| 3701 | ACTCCGGGTG                | AGCATTCATC  | AGGCGGGCAA  | GAATGTGAAT | AAAGGCCGGA |
|      | TGAGGCCAC                 | TCGTAAGTAG  | TCCGCCCGTT  | CTTACACTTA | TTTCCGGCCT |
| 3751 | TAAAACTTGT                | GCTTATTTTT  | CTTTACGGTC  | TTTAAAAAGG | CCGTAATATC |
|      | ATTTTGAACA                | CGAATAAAAA  | GAAATGCCAG  | AAATTTTCC  | GGCATTATAG |
| 3801 | CAGCTGAACG                | GTCTGGTTAT  | AGGTACATTG  | AGCAACTGAC | TGAAATGCCT |
|      | GTCGACTTGC                | CAGACCAATA  | TCCATGTAAC  | TCGTTGACTG | ACTTTACGGA |
| 3851 | CAAATGTTC                 | TTTACGATGC  | CATTGGGATA  | TATCAACGGT | GGTATATCCA |
|      | GTTTTACAAG                | AAATGCTACG  | GTAACCCTAT  | ATAGTTGCCA | CCATATAGGT |
| 3901 | GTGATTTTTT                | TCTCCATTTT  | AGCTTCCTTA  | GCTCCTGAAA | ATCTCGATAA |
|      | CACTAAAAAA                | AGAGGTAAAA  | TCGAAGGAAT  | CGAGGACTTT | TAGAGCTATT |
| 3951 | CTCAAAAAAT                | ACGCCCCGGTA | GTGATCTTAT  | TTCATTATGG | TGAAAGTTGG |
|      | GAGTTTTTTA                | TGCGGGCCAT  | CACTAGAATA  | AAGTAATACC | ACTTTCAACC |
| 4001 | AACCTCACCC                | GACGTCTAAT  | GTGAGTTAGC  | TCACTCATTA | GGCACCCAG  |
|      | TTGGAGTGGG                | CTGCAGATTA  | CACTCAATCG  | AGTGAGTAAT | CCGTGGGGTC |
| 4051 | GCTTTACACT                | TTATGCTTCC  | GGCTCGTATG  | TTGTGTGGAA | TTGTGAGCGG |
|      | CGAAATGTGA                | AATACGAAGG  | CCGAGCATAAC | AACACACCTT | AACACTCGCC |
|      | M13 Reverse primer 100.0% |             |             |            |            |
|      | =====                     |             |             |            |            |
| 4101 | ATAACAATTT                | CACACAGGAA  | ACAGCTATGA  | CCATGATTAC | GAATT      |
|      | TATTGTTAAA                | GTGTGTCCTT  | TGTCGATACT  | GGTACTAATG | CTTAA      |

Fig. 14 (cont.)

MS-GPC-1:

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
QYGHRGGFDHWGQGTLVTVSS (SEQ ID NO: 37)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFNESVF  
GGGTKLTVLG (SEQ ID NO: 38)

MS-GPC-6

VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWV  
SAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR  
GYGRYSPDLWGQGTLVTVSS (SEQ ID NO: 39)

VL

DIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY  
GASSRATGVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNLPFTFG  
QGTEKVEIKRT (SEQ ID NO: 40)

MS-GPC-8

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

Fig. 15

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMPQAV  
FGGGTKLTVLG (SEQ ID NO: 42)

MS-GPC-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
QLHYRGGFDLWGQGTLVTVSS (SEQ ID NO: 43)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLTMGVF  
GGGTKLTVLG (SEQ ID NO: 44)

MS-GPC-8-6

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 46)

MS-GPC-8-10

VH

Fig. 15 (cont.)

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVF  
GGGTKLTVLG (SEQ ID NO: 48)

MS-GPC-8-17

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSIVYVF  
GGGTKLTVLG (SEQ ID NO: 50)

MS-GPC-8-27

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

Fig. 15 (cont.)

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV  
FGGGTKLTVLG (SEQ ID NO: 52)

MS-GPC-8-6-13

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGANYVTWYQQLPGTAPKLLIYD  
NNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFG  
GGTKLTVLG (SEQ ID NO: 54)

MS-GPC-8-10-57

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVQWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVF  
GGGTKLTVLG (SEQ ID NO: 56)

MS-GPC-8-27-41

VH

Fig. 15 (cont.)

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVQWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV  
FGGGTKLTVLG (SEQ ID NO: 58)

MS-GPC-8-1

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSHYVF  
GGGTKLTVLG (SEQ ID NO: 28)

MS-GPC-8-9

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDIQLHVF  
GGGTKLTVLG (SEQ ID NO: 31)

Fig. 15 (cont.)

MS-GPC-8-18

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSIIYVF  
GGGTKLTVLG (SEQ ID NO: 32)

MS-GPC-8-6-2

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGSNYVHWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 45)

MS-GPC-8-6-19

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

Fig. 15 (cont.)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGSNYVAWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 47)

MS-GPC-8-6-27

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSDSNIGANYVTWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 49)

MS-GPC-8-6-45

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSEPNIGSNYVFWYQQLPGTAPKLLIYD  
NNQRPSGVPDRFSGSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFG  
GGTKLTVLG (SEQ ID NO: 51)

MS-GPC-8-6-47

Fig. 15 (cont.)



VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVLTMTNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGSNYVSWYQQLPGTSPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 53)

MS-GPC-8-27-7

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVLTMTNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVGWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV  
FGGGTKLTVLG (SEQ ID NO: 55)

MS-GPC-8-27-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDDKYYSTSLKTRLTISKDTSKNQVLTMTNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

Fig. 15 (cont.)

DIVLTQPPSVSGAPGQRVTISCSGSESNIGANYVNWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV  
FGGGTKLTVLG (SEQ ID NO: 57)

Fig. 15 (cont.)

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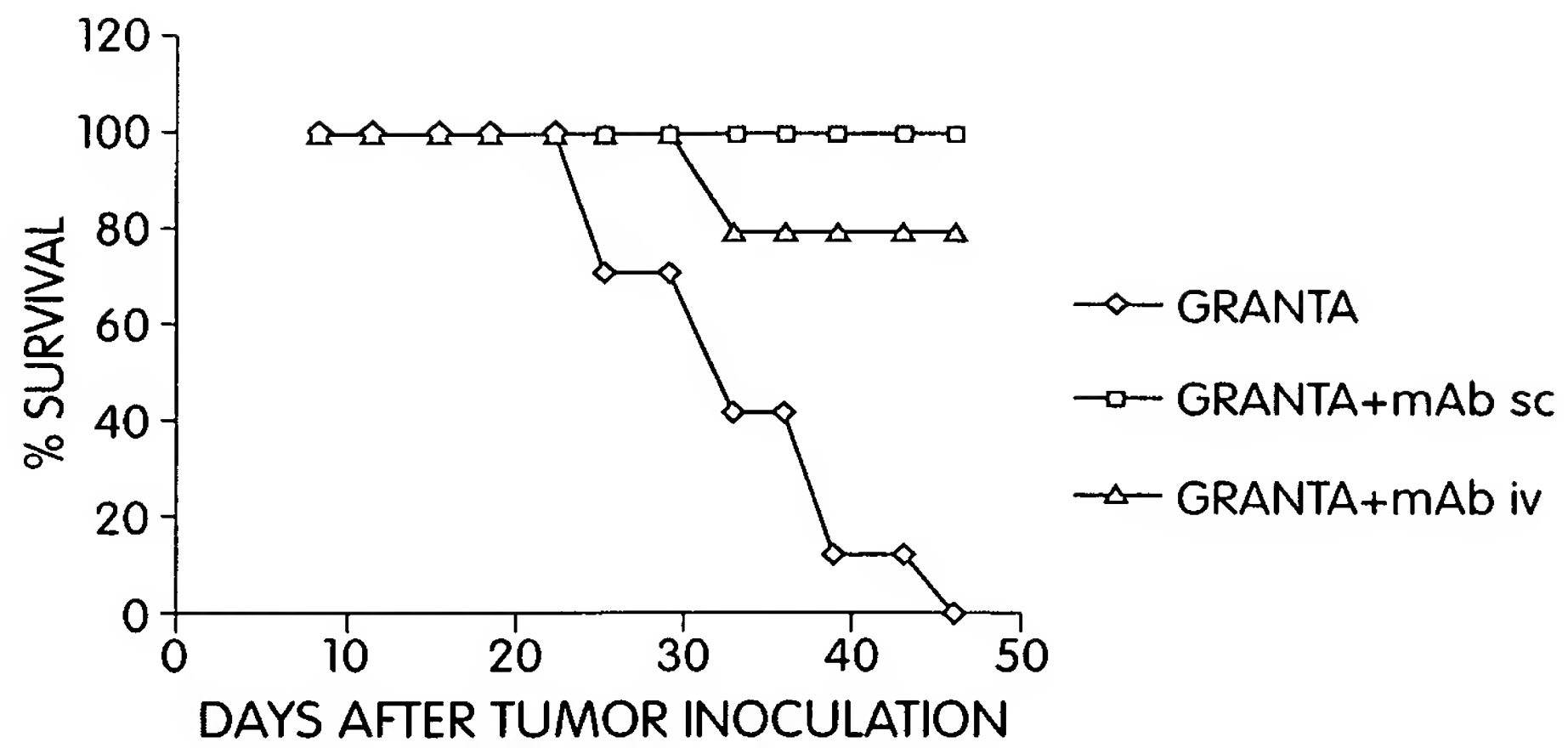


Fig. 16A

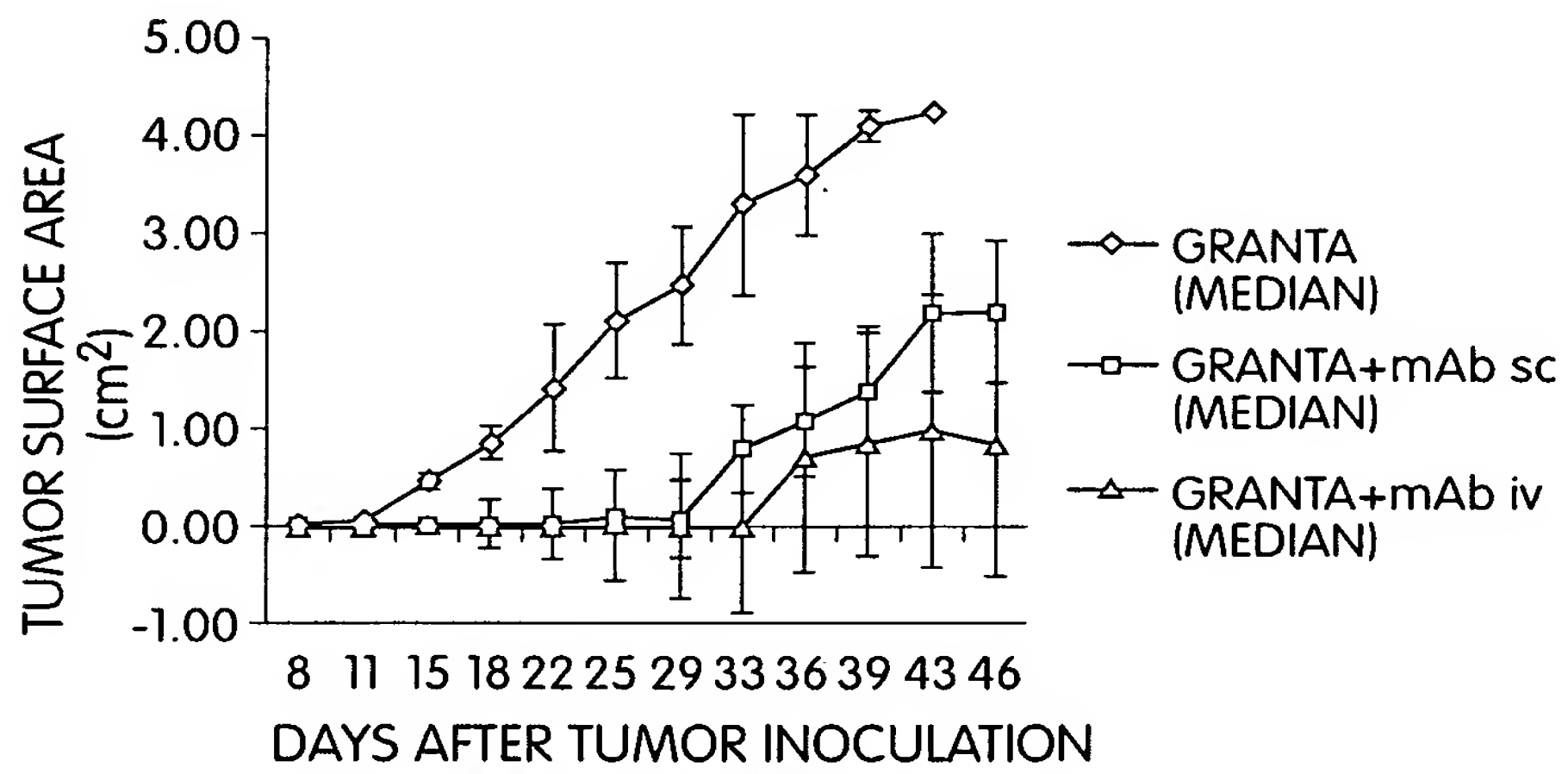


Fig. 16B

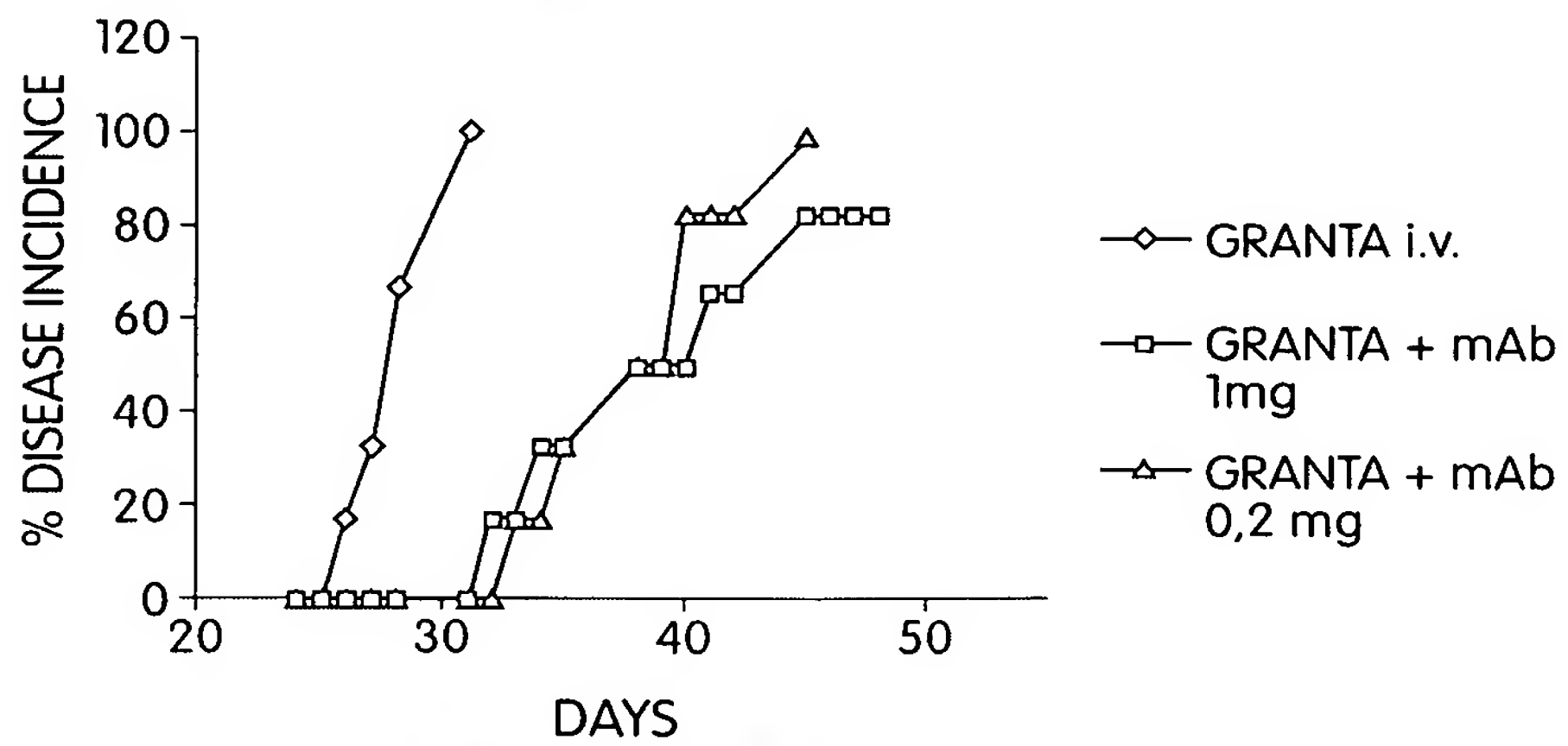


Fig. 16C



MOUSE #2, UNTREATED, DAY 32; TUMOR AREA 4.76 cm<sup>2</sup>

Fig. 16D



MOUSE #13, mAb i.v., DAY 32; TUMOR AREA 0.01 cm<sup>2</sup>

Fig. 16E